

Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys Glu Lys Phe Glu Cys
 290 295 300
 Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn Arg Asn His Gln Asp
 305 310 315 320
 Pro Leu Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met
 325 330 335
 Asn Glu Ala Lys Asp Phe Tyr Leu Ala Thr Ser Pro Pro Asp Ser Phe
 340 345 350
 Leu Asp Asp His His Leu Thr Arg Pro His Pro Glu Arg Val Pro Phe
 355 360 365
 Leu Val Ala Glu Thr Pro Arg Ala Arg His Thr Leu Asp Glu Leu Asn
 370 375 380
 Pro Gln Lys Ser Lys His Gln Gly Val Arg Lys Ala Lys Trp His Leu
 385 390 395 400
 Gly Ile Arg Ser Gln Ser Arg Pro Asn Asp Ile Met Ala Glu Val Cys
 405 410 415
 Arg Ala Ile Lys Gln Leu Asp Tyr Glu Trp Lys Val Val Asn Pro Tyr
 420 425 430
 Tyr Leu Arg Val Arg Arg Lys Asn Pro Val Thr Ser Thr Tyr Ser Lys
 435 440 445
 Met Ser Leu Gln Leu Tyr Gln Val Asp Ser Arg Thr Tyr Leu Leu Asp
 450 455 460
 Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu Ala Lys Ser Gly Thr Ala
 465 470 475 480
 Thr Pro Gln Arg Ser Gly Ser Val Ser Asn Tyr Arg Ser Cys Gln Arg
 485 490 495
 Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys Ser Ser Glu Val Ser Leu
 500 505 510
 Thr Ser Ser Val Thr Ser Leu Asp Ser Ser Pro Val Asp Leu Thr Pro
 515 520 525
 Arg Pro Gly Ser His Thr Ile Glu Phe Phe Glu Met Cys Ala Asn Leu
 530 535 540
 Ile Lys Ile Leu Ala Gln
 545 550

<210> SEQ ID NO 2

<211> LENGTH: 550

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Met Ala Thr Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly
 1 5 10 15
 His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val
 20 25 30
 Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile
 35 40 45
 Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg
 50 55 60
 Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys
 65 70 75 80
 Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu
 85 90 95
 Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg
 100 105 110
 Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly
 115 120 125
 Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro
 130 135 140

Glu	Asn	Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe
145					150					155					160
Gly	Leu	Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys
				165					170						175
Gly	Ser	Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr
				180				185					190		
Ala	Gly	Pro	Glu	Val	Asp	Ile	Trp	Ser	Ser	Gly	Val	Ile	Leu	Tyr	Ala
		195					200					205			
Leu	Leu	Cys	Gly	Thr	Leu	Pro	Phe	Asp	Asp	Asp	His	Val	Pro	Thr	Leu
	210					215				220					
Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn
	225				230					235					240
Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met
				245					250						255
Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln
				260				265							270
Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr
		275					280					285			
Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys
		290				295					300				
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp
				310						315					320
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met
				325					330						335
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe
				340				345							350
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe
		355					360					365			
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn
		370				375					380				
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu
				390						395					400
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys
				405					410						415
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr
				420				425					430		
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys
		435					440					445			
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp
		450				455					460				
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala
		465			470					475					480
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg
				485					490						495
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu
				500				505					510		
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro
		515					520					525			
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu
		530				535						540			
Ile	Lys	Ile	Leu	Ala	Gln										
		545				550									

210> SEQ ID NO 3

<211> LENGTH: 550

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met	Ala	Thr	Ala	Glu	Lys	Gln	Lys	His	Asp	Gly	Arg	Val	Lys	Ile	Gly		
1				5					10						15		
His	Tyr	Ile	Leu	Gly	Asp	Thr	Leu	Gly	Val	Gly	Thr	Phe	Gly	Lys	Val		
			20					25					30				
Lys	Val	Gly	Lys	His	Glu	Leu	Thr	Gly	His	Lys	Val	Ala	Val	Lys	Ile		
		35					40					45					
Leu	Asn	Arg	Gln	Lys	Ile	Arg	Ser	Leu	Asp	Val	Val	Gly	Lys	Ile	Arg		
	50					55				60							
Arg	Glu	Ile	Gln	Asn	Leu	Lys	Leu	Phe	Arg	His	Pro	His	Ile	Ile	Lys		
65				70				75						80			
Leu	Tyr	Gln	Val	Ile	Ser	Thr	Pro	Ser	Asp	Ile	Phe	Met	Val	Met	Glu		
		85						90					95				
Tyr	Val	Ser	Gly	Glu	Leu	Phe	Asp	Tyr	Ile	Cys	Lys	Asn	Gly	Arg			
		100					105					110					
Leu	Asp	Glu	Lys	Glu	Ser	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Gly		
	115					120						125					
Val	Asp	Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro		
	130					135					140						
Glu	Asn	Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe		
145				150					155					160			
Gly	Leu	Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys		
		165						170					175				
Gly	Ser	Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr		
		180					185					190					
Ala	Gly	Pro	Glu	Val	Asp	Ile	Trp	Ser	Ser	Gly	Val	Ile	Leu	Tyr	Ala		
	195					200						205					
Leu	Leu	Cys	Gly	Thr	Leu	Phe	Asp	Asp	Asp	His	Val	Pro	Thr	Leu			
	210				215					220							
Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn		
225				230					235					240			
Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met		
		245						250					255				
Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln		
	260						265					270					
Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr		
	275					280					285						
Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys		
	290					295				300							
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp		
305				310					315					320			
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met		
		325						330					335				
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe		
	340						345					350					
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe		
	355					360					365						
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn		
	370				375					380							
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu		
385				390					395					400			
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys		
		405						410					415				
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr		
	420						425					430					
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys		
	435					440				445							
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp		

450					455					460							
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala		
465					470					475					480		
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg		
				485						490					495		
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu		
			500					505					510				
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro		
		515					520					525					
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu		
	530					535					540						
Ile	Lys	Ile	Leu	Ala	Gln												
545					550												

<210> SEQ ID NO 4

<211> LENGTH: 520

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Gly	Glu	His	Gln	Leu	Thr	Gly	His	Lys	Val	Ala	Val	Lys	Ile	Leu	Asn		
1			5					10					15				
Arg	Gln	Lys	Ile	Arg	Ser	Leu	Asp	Val	Val	Gly	Lys	Ile	Lys	Arg	Glu		
			20					25					30				
Ile	Gln	Asn	Leu	Lys	Leu	Phe	Arg	His	Pro	His	Ile	Ile	Lys	Leu	Tyr		
		35				40						45					
Gln	Val	Ile	Ser	Thr	Pro	Thr	Asp	Phe	Phe	Met	Val	Met	Glu	Tyr	Val		
	50					55				60							
Ser	Gly	Gly	Glu	Leu	Phe	Asp	Tyr	Ile	Cys	Lys	His	Gly	Arg	Val	Glu		
65				70					75					80			
Glu	Met	Glu	Ala	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Ala	Val	Asp		
			85					90						95			
Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn		
		100						105					110				
Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe	Gly	Leu		
		115				120						125					
Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys	Gly	Ser		
	130				135						140						
Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr	Ala	Gly		
145			150						155					160			
Pro	Glu	Val	Asp	Ile	Trp	Ser	Cys	Gly	Val	Ile	Leu	Tyr	Ala	Leu	Leu		
			165					170						175			
Cys	Gly	Thr	Leu	Pro	Phe	Asp	Asp	Glu	His	Val	Pro	Thr	Leu	Phe	Lys		
		180					185						190				
Lys	Ile	Arg	Gly	Gly	Val	Phe	Tyr	Ile	Pro	Glu	Tyr	Leu	Asn	Arg	Ser		
		195				200						205					
Val	Ala	Thr	Leu	Leu	Met	His	Met	Leu	Gln	Val	Asp	Pro	Leu	Lys	Arg		
	210				215						220						
Ala	Thr	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln	Asp	Leu		
225				230						235				240			
Pro	Ser	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Asp	Ala	Asn	Val	Ile		
			245					250						255			
Asp	Asp	Glu	Ala	Val	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys	Thr	Glu		
		260					265						270				
Ser	Glu	Val	Met	Asn	Ser	Leu	Tyr	Ser	Gly	Asp	Pro	Gln	Asp	Gln	Leu		
	275					280						285					
Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met	Asn	Gln		
	290				295						300						
Ala	Ser	Glu	Phe	Tyr	Leu	Ala	Ser	Ser	Pro	Ser	Gly	Ser	Phe	Met			

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305          310          315          320
Asp Asp Ser Ala Met His Ile Pro Pro Gly Leu Lys Pro His Pro Glu
          325          330          335
Arg Met Pro Pro Leu Ile Ala Asp Ser Pro Lys Ala Arg Cys Pro Leu
          340          345          350
Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val Lys Lys Ala
          355          360          365
Lys Trp His Leu Gly Ile Arg Ser Gln Ser Lys Pro Tyr Asp Ile Met
          370          375          380
Ala Glu Val Tyr Arg Ala Met Lys Gln Leu Asp Phe Glu Trp Lys Val
385          390          395          400
Val Asn Ala Tyr His Leu Arg Val Arg Arg Lys Asn Pro Val Thr Gly
          405          410          415
Asn Tyr Val Lys Met Ser Leu Gln Leu Tyr Leu Val Asp Asn Arg Ser
          420          425          430
Tyr Leu Leu Asp Phe Lys Ser Ile Asp Asp Glu Val Val Glu Gln Arg
          435          440          445
Ser Gly Ser Ser Thr Pro Gln Arg Ser Cys Ser Ala Ala Gly Leu His
          450          455          460
Arg Pro Arg Ser Ser Phe Asp Ser Thr Thr Ala Glu Ser His Ser Leu
465          470          475          480
Ser Gly Ser Leu Thr Gly Ser Leu Thr Gly Ser Thr Leu Ser Ser Val
          485          490          495
Ser Pro Arg Leu Gly Ser His Thr Met Asp Phe Phe Glu Met Cys Ala
          500          505          510
Ser Leu Ile Thr Thr Leu Ala Arg
          515          520

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<210> SEQ ID NO 5

<211> LENGTH: 552

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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Met Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly His Tyr
1          5          10          15
Val Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val Lys Ile
          20          25          30
Gly Glu His Gln Leu Thr Gly His Lys Val Ala Val Lys Ile Leu Asn
          35          40          45
Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Lys Arg Glu
          50          55          60
Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr
65          70          75          80
Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val
          85          90          95
Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu
          100          105          110
Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp
          115          120          125
Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn
          130          135          140
Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu
145          150          155          160
Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser
          165          170          175
Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly
          180          185          190
Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu

```


50						55						60					
Glu	Val	Leu	Asp	Ser	Glu	Thr	Leu	Cys	Arg	Arg	Ala	Val	Lys	Ile	Leu		
65					70					75					80		
Lys	Lys	Lys	Lys	Leu	Arg	Arg	Ile	Pro	Asn	Gly	Glu	Ala	Asn	Val	Lys		
				85					90					95			
Lys	Glu	Ile	Gln	Leu	Leu	Arg	Arg	Leu	Arg	His	Lys	Asn	Val	Ile	Gln		
			100					105					110				
Leu	Val	Asp	Val	Leu	Tyr	Asn	Glu	Glu	Lys	Gln	Lys	Met	Tyr	Met	Val		
		115				120						125					
Met	Glu	Tyr	Cys	Val	Cys	Gly	Met	Gln	Glu	Met	Leu	Asp	Ser	Val	Pro		
		130				135					140						
Glu	Lys	Arg	Phe	Pro	Val	Cys	Gln	Ala	His	Gly	Tyr	Phe	Cys	Gln	Leu		
145					150					155					160		
Ile	Asp	Gly	Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Ile	Val	His	Lys	Asp		
			165					170						175			
Ile	Lys	Pro	Gly	Asn	Leu	Leu	Leu	Thr	Thr	Gly	Gly	Thr	Leu	Lys	Ile		
			180					185					190				
Ser	Asp	Leu	Gly	Val	Ala	Glu	Ala	Leu	His	Pro	Phe	Ala	Ala	Asp	Asp		
		195						200				205					
Thr	Cys	Arg	Thr	Ser	Gln	Gly	Ser	Pro	Ala	Phe	Gln	Pro	Pro	Glu	Ile		
		210				215						220					
Ala	Asn	Gly	Leu	Asp	Thr	Phe	Ser	Gly	Phe	Lys	Val	Asp	Ile	Trp	Ser		
225					230					235				240			
Ala	Gly	Val	Thr	Leu	Tyr	Asn	Ile	Thr	Thr	Gly	Leu	Tyr	Pro	Phe	Glu		
			245							250				255			
Gly	Asp	Asn	Ile	Tyr	Lys	Leu	Phe	Glu	Asn	Ile	Gly	Lys	Gly	Ser	Tyr		
		260						265					270				
Ala	Ile	Pro	Gly	Asp	Cys	Gly	Pro	Leu	Ser	Asp	Leu	Leu	Lys	Gly			
		275				280					285						
Met	Leu	Glu	Tyr	Glu	Pro	Ala	Lys	Arg	Phe	Ser	Ile	Arg	Gln	Ile	Arg		
		290				295					300						
Gln	His	Ser	Trp	Phe	Arg	Lys	Lys	His	Pro	Pro	Ala	Glu	Ala	Pro	Val		
305					310					315				320			
Pro	Ile	Pro	Pro	Ser	Pro	Asp	Thr	Lys	Asp	Arg	Trp	Arg	Ser	Met	Thr		
				325					330					335			
Val	Val	Pro	Tyr	Leu	Glu	Asp	Leu	His	Gly	Ala	Asp	Glu	Asp	Glu	Asp		
			340					345					350				
Leu	Phe	Asp	Ile	Glu	Asp	Asp	Ile	Ile	Tyr	Thr	Gln	Asp	Phe	Thr	Val		
		355					360					365					
Pro	Gly	Gln	Val	Pro	Glu	Glu	Ala	Ser	His	Asn	Gly	Gln	Arg	Arg			
		370				375				380							
Gly	Leu	Pro	Lys	Ala	Val	Cys	Met	Asn	Gly	Thr	Glu	Ala	Ala	Gln	Leu		
385					390					395				400			
Ser	Thr	Lys	Ser	Arg	Ala	Glu	Gly	Arg	Ala	Pro	Asn	Pro	Ala	Arg	Lys		
				405					410					415			
Ala	Cys	Ser	Ala	Ser	Ser	Lys	Ile	Arg	Arg	Leu	Ser	Ala	Cys	Lys	Gln		
			420					425					430				

Gln

<210> SEQ ID NO 7

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met	Glu	Val	Val	Asp	Pro	Gln	Gln	Leu	Gly	Met	Phe	Thr	Glu	Gly	Glu		
1				5					10					15			
Leu	Met	Ser	Val	Gly	Met	Asp	Thr	Phe	Ile	His	Arg	Ile	Asp	Ser	Thr		
			20					25					30				

Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
 35 40 45
 Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
 50 55 60
 Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
 65 70 75 80
 Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys
 85 90 95
 Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln
 100 105 110
 Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val
 115 120 125
 Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro
 130 135 140
 Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu
 145 150 155 160
 Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp
 165 170 175
 Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile
 180 185 190
 Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp
 195 200 205
 Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile
 210 215 220
 Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
 225 230 235 240
 Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
 245 250 255
 Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr
 260 265 270
 Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly
 275 280 285
 Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
 290 295 300
 Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val
 305 310 315 320
 Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
 325 330 335
 Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp
 340 345 350
 Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val
 355 360 365
 Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg
 370 375 380
 Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu
 385 390 395 400
 Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys
 405 410 415
 Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln
 420 425 430

Gln

<210> SEQ ID NO 8

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu

1				5						10					15
Leu	Met	Ser	Val	Gly	Met	Asp	Thr	Phe	Ile	His	Arg	Ile	Asp	Ser	Thr
			20					25					30		
Glu	Val	Ile	Tyr	Gln	Pro	Arg	Arg	Lys	Arg	Ala	Lys	Leu	Ile	Gly	Lys
		35					40					45			
Tyr	Leu	Met	Gly	Asp	Leu	Leu	Gly	Glu	Gly	Ser	Tyr	Gly	Lys	Val	Lys
	50					55					60				
Glu	Val	Leu	Asp	Ser	Glu	Thr	Leu	Cys	Arg	Arg	Ala	Val	Lys	Ile	Leu
	65					70				75				80	
Lys	Lys	Lys	Lys	Lys	Arg	Arg	Ile	Pro	Asn	Gly	Glu	Ala	Asn	Val	Lys
				85					90				95		
Lys	Glu	Ile	Gln	Leu	Leu	Arg	Arg	Leu	Arg	His	Lys	Asn	Val	Ile	Gln
			100					105					110		
Leu	Val	Asp	Val	Leu	Tyr	Asn	Glu	Glu	Lys	Gln	Lys	Met	Tyr	Met	Val
		115					120					125			
Met	Glu	Tyr	Cys	Val	Cys	Gly	Met	Gln	Glu	Met	Leu	Asp	Ser	Val	Pro
	130					135					140				
Glu	Lys	Arg	Phe	Pro	Val	Cys	Gln	Ala	His	Gly	Tyr	Phe	Cys	Gln	Leu
				150						155				160	
Ile	Asp	Gly	Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Ile	Val	His	Lys	Asp
				165					170					175	
Ile	Lys	Pro	Gly	Asn	Leu	Leu	Leu	Thr	Thr	Gly	Gly	Thr	Leu	Lys	Ile
			180					185					190		
Ser	Asp	Leu	Gly	Val	Ala	Glu	Ala	Leu	His	Pro	Phe	Ala	Ala	Asp	Asp
		195					200					205			
Thr	Cys	Arg	Thr	Ser	Gln	Gly	Ser	Pro	Ala	Phe	Gln	Pro	Pro	Glu	Ile
		210				215					220				
Ala	Asn	Gly	Leu	Asp	Thr	Phe	Ser	Gly	Phe	Lys	Val	Asp	Ile	Trp	Ser
				230						235				240	
Ala	Gly	Val	Thr	Leu	Tyr	Asn	Ile	Thr	Thr	Gly	Leu	Tyr	Pro	Phe	Glu
			245						250					255	
Gly	Asp	Asn	Ile	Tyr	Lys	Leu	Phe	Glu	Asn	Ile	Gly	Lys	Gly	Ser	Tyr
			260					265					270		
Ala	Ile	Pro	Gly	Asp	Cys	Gly	Pro	Pro	Leu	Ser	Asp	Leu	Leu	Lys	Gly
		275					280					285			
Met	Leu	Glu	Tyr	Glu	Pro	Ala	Lys	Arg	Phe	Ser	Ile	Arg	Gln	Ile	Arg
		290				295					300				
Gln	His	Ser	Trp	Phe	Arg	Lys	Lys	His	Pro	Pro	Ala	Glu	Ala	Pro	Val
				310						315				320	
Pro	Ile	Pro	Pro	Ser	Pro	Asp	Thr	Lys	Asp	Arg	Trp	Arg	Ser	Met	Thr
				325					330					335	
Val	Val	Pro	Tyr	Leu	Glu	Asp	Leu	His	Gly	Ala	Asp	Glu	Asp	Glu	Asp
			340					345				350			
Leu	Phe	Asp	Ile	Glu	Asp	Asp	Ile	Ile	Tyr	Thr	Gln	Asp	Phe	Thr	Val
		355					360					365			
Pro	Gly	Gln	Val	Pro	Glu	Glu	Glu	Ala	Ser	His	Asn	Gly	Gln	Arg	Arg
		370				375					380				
Gly	Leu	Pro	Lys	Ala	Val	Cys	Met	Asn	Gly	Thr	Glu	Ala	Ala	Gln	Leu
				390						395				400	
Ser	Thr	Lys	Ser	Arg	Ala	Glu	Gly	Arg	Ala	Pro	Asn	Pro	Ala	Arg	Lys
				405					410					415	
Ala	Cys	Ser	Ala	Ser	Ser	Lys	Ile	Arg	Arg	Leu	Ser	Ala	Cys	Lys	Gln
			420					425					430		

Gln

<210> SEQ ID NO 9

<211> LENGTH: 431

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

```
Met Ser Phe Leu Val Ser Lys Pro Glu Arg Ile Arg Arg Trp Val Ser
1          5          10          15
Glu Lys Phe Ile Val Glu Gly Leu Arg Asp Leu Glu Leu Phe Gly Glu
20          25          30
Gln Pro Pro Gly Asp Thr Arg Arg Lys Thr Asn Asp Ala Ser Ser Glu
35          40          45
Ser Ile Ala Ser Phe Ser Lys Gln Glu Val Met Ser Ser Phe Leu Pro
50          55          60
Glu Gly Gly Cys Tyr Glu Leu Leu Thr Val Ile Gly Lys Gly Phe Glu
65          70          75          80
Asp Leu Met Thr Val Asn Leu Ala Arg Tyr Lys Pro Thr Gly Glu Tyr
85          90          95
Val Thr Val Arg Arg Ile Asn Leu Glu Ala Cys Ser Asn Glu Met Val
100         105         110
Thr Phe Leu Gln Gly Glu Leu His Val Ser Lys Leu Phe Asn His Pro
115         120         125
Asn Ile Val Pro Tyr Arg Ala Thr Phe Ile Ala Asp Asn Glu Leu Trp
130         135         140
Val Val Thr Ser Phe Met Ala Tyr Gly Ser Ala Lys Asp Leu Ile Cys
145         150         155         160
Thr His Phe Met Asp Gly Met Asn Glu Leu Ala Ile Ala Tyr Ile Leu
165         170         175
Gln Gly Val Leu Lys Ala Leu Asp Tyr Ile His His Met Gly Tyr Val
180         185         190
His Arg Ser Val Lys Ala Ser His Ile Leu Ile Ser Val Asp Gly Lys
195         200         205
Val Tyr Leu Ser Gly Leu Arg Ser Asn Leu Ser Met Ile Ser His Gly
210         215         220
Gln Arg Gln Arg Val Val His Asp Phe Pro Lys Tyr Ser Val Lys Val
225         230         235         240
Leu Pro Trp Leu Ser Pro Glu Val Leu Gln Gln Asn Leu Gln Gly Tyr
245         250         255
Asp Ala Lys Ser Asp Ile Tyr Ser Val Gly Ile Thr Ala Cys Glu Leu
260         265         270
Ala Asn Gly His Val Pro Phe Lys Asp Met Pro Ala Thr Gln Met Leu
275         280         285
Leu Glu Lys Leu Asn Gly Thr Val Pro Cys Leu Leu Asp Thr Ser Thr
290         295         300
Ile Pro Ala Glu Glu Leu Thr Met Ser Pro Ser Arg Ser Val Ala Asn
305         310         315         320
Ser Gly Leu Ser Asp Ser Leu Thr Thr Ser Thr Pro Arg Pro Ser Asn
325         330         335
Gly Asp Trp Pro Ser His Pro Tyr His Arg Thr Phe Ser Pro His Phe
340         345         350
His His Phe Val Glu Gln Cys Leu Gln Arg Asn Pro Asp Ala Arg Pro
355         360         365
Ser Ala Ser Thr Leu Leu Asn His Ser Phe Phe Lys Gln Ile Lys Arg
370         375         380
Arg Ala Ser Lys Ala Leu Pro Glu Leu Leu Arg Pro Val Thr Pro Ile
385         390         395         400
Thr Asn Phe Glu Gly Ser Gln Ser Gln Asp His Ser Gly Ile Phe Gly
405         410         415
Leu Val Thr Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Phe
420         425         430
```

<210> SEQ ID NO 10

<211> LENGTH: 418

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

```
Met Ser Leu Leu Asp Cys Phe Cys Thr Ser Arg Thr Gln Val Glu Ser
1      5      10      15
Leu Arg Pro Glu Lys Gln Ser Glu Thr Ser Ile His Gln Tyr Leu Val
20      25      30
Asp Glu Pro Thr Leu Ser Trp Ser Arg Pro Ser Thr Arg Ala Ser Glu
35      40      45
Val Leu Cys Ser Thr Asn Val Ser His Tyr Glu Leu Gln Val Glu Ile
50      55      60
Gly Arg Gly Phe Asp Asn Leu Thr Ser Val His Leu Ala Arg His Thr
65      70      75
Pro Thr Gly Thr Leu Val Thr Ile Lys Ile Thr Asn Leu Glu Asn Cys
85      90      95
Asn Glu Glu Arg Leu Lys Ala Leu Gln Lys Ala Val Ile Leu Ser His
100     105     110
Phe Phe Arg His Pro Asn Ile Thr Thr Tyr Trp Thr Val Phe Thr Val
115     120     125
Gly Ser Trp Leu Trp Val Ile Ser Pro Phe Met Ala Tyr Gly Ser Ala
130     135     140
Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu Thr Leu
145     150     155     160
Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr Leu His
165     170     175
Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile Leu Ile
180     185     190
Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu His Ser
195     200     205
Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe Pro Gln
210     215     220
Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu Arg Gln
225     230     235     240
Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val Gly Ile
245     250     255
Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp Met His
260     265     270
Arg Thr Gln Met Leu Leu Gln Lys Leu Lys Gly Pro Pro Tyr Ser Pro
275     280     285
Leu Asp Ile Ser Ile Phe Pro Gln Ser Glu Ser Arg Met Lys Asn Ser
290     295     300
Gln Ser Gly Val Asp Ser Gly Ile Gly Glu Ser Val Leu Val Ser Ser
305     310     315     320
Gly Thr His Thr Val Asn Ser Asp Arg Leu His Thr Pro Ser Ser Lys
325     330     335
Thr Phe Ser Pro Ala Phe Phe Ser Leu Val Gln Leu Cys Leu Gln Gln
340     345     350
Asp Pro Glu Lys Arg Pro Ser Ala Ser Ser Leu Leu Ser His Val Phe
355     360     365
Phe Lys Gln Met Lys Glu Glu Ser Gln Asp Ser Ile Leu Ser Leu Leu
370     375     380
Pro Pro Ala Tyr Asn Lys Pro Ser Ile Ser Leu Pro Pro Val Leu Pro
385     390     395     400
Trp Thr Glu Pro Glu Cys Asp Phe Pro Asp Glu Lys Asp Ser Tyr Trp
405     410     415
Glu Phe
```

210> SEQ ID NO 11

<211> LENGTH: 341

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Pro Phe Pro Phe Gly Lys Ser His Lys Ser Pro Ala Asp Ile Val
1 5 10 15
Lys Asn Leu Lys Glu Ser Met Ala Val Leu Glu Lys Gln Asp Ile Ser
20 25 30
Asp Lys Lys Ala Glu Lys Ala Thr Glu Glu Val Ser Lys Asn Leu Val
35 40 45
Ala Met Lys Glu Ile Leu Tyr Gly Thr Asn Glu Lys Glu Pro Gln Thr
50 55 60
Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr Asn Ser Gly Leu Leu
65 70 75 80
Ser Thr Leu Val Ala Asp Leu Gln Leu Ile Asp Phe Glu Gly Lys Lys
85 90 95
Asp Val Ala Gln Ile Phe Asn Asn Ile Leu Arg Arg Gln Ile Gly Thr
100 105 110
Arg Thr Pro Thr Val Glu Tyr Ile Cys Thr Gln Gln Asn Ile Leu Phe
115 120 125
Met Leu Leu Lys Gly Tyr Glu Ser Pro Glu Ile Ala Leu Asn Cys Gly
130 135 140
Ile Met Leu Arg Glu Cys Ile Arg His Glu Pro Leu Ala Lys Ile Ile
145 150 155 160
Leu Trp Ser Glu Gln Phe Tyr Asp Phe Phe Arg Tyr Val Glu Met Ser
165 170 175
Thr Phe Asp Ile Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu
180 185 190
Thr Arg His Lys Leu Leu Ser Ala Glu Phe Leu Glu Gln His Tyr Asp
195 200 205
Arg Phe Phe Ser Glu Tyr Glu Lys Leu Leu His Ser Glu Asn Tyr Val
210 215 220
Thr Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
225 230 235 240
His Asn Phe Thr Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu
245 250 255
Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Phe
260 265 270
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Thr
275 280 285
Gln Pro Ile Leu Asp Ile Leu Leu Lys Asn Gln Ala Lys Leu Ile Glu
290 295 300
Phe Leu Ser Lys Phe Gln Asn Asp Arg Thr Glu Asp Glu Gln Phe Asn
305 310 315 320
Asp Glu Lys Thr Tyr Leu Val Lys Gln Ile Arg Asp Leu Lys Arg Pro
325 330 335
Ala Gln Gln Glu Ala
340

<210> SEQ ID NO 12

<211> LENGTH: 337

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Lys Lys Met Pro Leu Phe Ser Lys Ser His Lys Asn Pro Ala Glu
1 5 10 15
Ile Val Lys Ile Leu Lys Asp Asn Leu Ala Ile Leu Glu Lys Gln Asp

Cys Lys Lys Asp Val Ala Ser Val Phe Asn Asn Leu Leu Arg Arg Gln
 100 105 110
 Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr Leu Ala Ala Arg Pro Glu
 115 120 125
 Ile Leu Ile Thr Leu Leu Leu Gly Tyr Glu Gln Pro Asp Ile Ala Leu
 130 135 140
 Thr Cys Gly Ser Met Leu Arg Glu Ala Val Arg His Glu His Leu Ala
 145 150 155 160
 Arg Ile Val Leu Tyr Ser Glu Tyr Phe Gln Arg Phe Phe Val Phe Val
 165 170 175
 Gln Ser Asp Val Phe Asp Ile Ala Thr Asp Ala Phe Ser Thr Phe Lys
 180 185 190
 Asp Leu Met Thr Lys His Lys Asn Met Cys Ala Glu Tyr Leu Asp Asn
 195 200 205
 Asn Tyr Asp Arg Phe Phe Gly Gln Tyr Ser Ala Leu Thr Asn Ser Glu
 210 215 220
 Asn Tyr Val Thr Arg Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu
 225 230 235 240
 Leu Asp Arg His Asn Phe Ser Thr Met Asn Lys Tyr Ile Thr Ser Pro
 245 250 255
 Glu Asn Leu Lys Thr Val Met Glu Leu Leu Arg Asp Lys Arg Arg Asn
 260 265 270
 Ile Gln Tyr Glu Ala Phe His Val Phe Lys Ile Phe Val Ala Asn Pro
 275 280 285
 Asn Lys Pro Arg Pro Ile Thr Asp Ile Leu Thr Arg Asn Arg Asp Lys
 290 295 300
 Leu Val Glu Phe Leu Thr Ala Phe His Asn Asp Arg Thr Asn Asp Glu
 305 310 315 320
 Gln Phe Asn Asp Glu Lys Ala Tyr Leu Ile Lys Gln Ile Gln Glu Leu
 325 330 335

Arg Val

<210> SEQ ID NO 14

<211> LENGTH: 636

<212> TYPE: PRT

<213> ORGANISM: *Caenorhabditis elegans*

<400> SEQUENCE: 14

Met Asp Ser Thr Thr Ser Leu Pro Asn Asn Val Leu Leu Lys Lys Ala
 1 5 10 15
 Arg Pro Ser Lys Ile Phe Ala Val Thr Ser Ala Asn Ala Leu Asn Val
 20 25 30
 Lys Thr Glu Pro Val Ile Phe Val Lys Ser Asp Asp Leu Asn Gln Ala
 35 40 45
 Asn Thr Pro Leu Thr Gly Ser Lys Phe Gly Thr His Leu Ala Cys Ile
 50 55 60
 Arg Thr Ser Cys Leu His Arg Thr Val Asn Ala Ser Asn Tyr Ser Thr
 65 70 75 80
 Met Ser Asp Gly Gly Leu Tyr Thr Ser Asp Glu Pro Cys Ser Ser Ala
 85 90 95
 Gln Ala Glu Phe Arg Leu Ala Ala His Trp Glu Ser Thr Phe Thr Arg
 100 105 110
 Thr Arg Glu Ile His Cys Asp Thr Gly Tyr Ser Ser Gln Ser Pro Pro
 115 120 125
 Glu Thr Thr Val Phe Ile Gln Lys Ser Arg Phe Pro Val Ala Glu Lys
 130 135 140
 Pro Gly Thr Pro Glu Leu Lys Ser Phe Glu Ser Lys Lys Leu Val Gln
 145 150 155 160
 Lys Lys Ser Gly Asn Ala Ser Thr Pro Thr Arg Lys Leu Ala Ser Glu

Glu	Lys		Lys	Ala	Lys	Asn	Thr	Ser	Met	Val	Lys	Gln	Thr	Pro	Ser	Lys	Leu
Lys	Ser	Pro	Lys	Ala	Leu	Lys	Met	Val	Lys	Lys	Glu	Asn	Glu	Pro	Ala		
Ile	Pro	Pro	Asn	His	Phe	Glu	Gly	Lys	Val	Tyr	Gly	Tyr	Leu	Val	Asp		
Asp	Met	Ser	Ala	Ile	Gly	Ile	Gln	Pro	Ile	Leu	Asp	Lys	Tyr	Asn	Glu		
Asp	Pro	Glu	Lys	Phe	Phe	Lys	Arg	Phe	Asp	Ser	Lys	Pro	Trp	Phe	Arg		
Arg	Lys	Val	Met	Pro	Leu	Leu	Phe	Gly	Lys	Ser	His	Lys	Ser	Pro	Ala		
Asp	Val	Val	Lys	Thr	Leu	Arg	Glu	Val	Leu	Thr	Ile	Leu	Asp	Lys	Leu		
Pro	Pro	Pro	Lys	Leu	Asp	Lys	Asp	Gly	Asn	Ile	Gln	Ser	Asp	Lys	Lys		
Tyr	Asp	Lys	Ala	Leu	Asp	Glu	Val	Ser	Lys	Asn	Val	Ala	Met	Ile	Lys		
Ser	Phe	Ile	Tyr	Gly	Asn	Asp	Ser	Ala	Glu	Pro	Ser	Ser	Glu	His	Val		
Val	Gln	Val	Ala	Gln	Leu	Ala	Gln	Glu	Val	Tyr	Asn	Ala	Asn	Ile	Leu		
Pro	Met	Leu	Ile	Lys	Met	Leu	Pro	Lys	Phe	Glu	Phe	Glu	Cys	Lys	Lys		
Asp	Val	Gly	Gln	Ile	Phe	Asn	Asn	Leu	Leu	Arg	Arg	Gln	Ile	Gly	Thr		
Arg	Ser	Pro	Thr	Val	Glu	Tyr	Leu	Gly	Ala	Arg	Pro	Glu	Ile	Leu	Ile		
Gln	Leu	Val	Gln	Gly	Tyr	Ser	Val	Pro	Asp	Ile	Ala	Leu	Thr	Cys	Glu		
Leu	Met	Leu	Arg	Glu	Ser	Ile	Arg	His	Asp	His	Leu	Ala	Lys	Ile	Ile		
Leu	Tyr	Ser	Asp	Val	Phe	Tyr	Pho	Phe	Phe	Leu	Tyr	Val	Gln	Ser	Glu		
Val	Phe	Asp	Ile	Ser	Ser	Asp	Ala	Phe	Ser	Thr	Phe	Lys	Glu	Leu	Thr		
Thr	Arg	His	Lys	Ala	Ile	Ile	Ala	Glu	Phe	Leu	Asp	Ser	Asn	Tyr	Asp		
Thr	Phe	Phe	Ala	Gln	Tyr	Gln	Asn	Leu	Leu	Asn	Ser	Lys	Asn	Tyr	Val		
Thr	Arg	Arg	Gln	Ser	Leu	Lys	Leu	Leu	Gly	Glu	Leu	Leu	Leu	Asp	Arg		
His	Asn	Phe	Asn	Thr	Met	Thr	Lys	Tyr	Ile	Ser	Asn	Pro	Asp	Asn	Leu		
Arg	Leu	Met	Met	Glu	Leu	Leu	Arg	Asp	Lys	Ser	Arg	Asn	Ile	Gln	Tyr		
Glu	Ala	Phe	His	Val	Phe	Lys	Val	Phe	Val	Ala	Asn	Pro	Asn	Lys	Pro		
Lys	Pro	Ile	Ser	Asp	Ile	Leu	Asn	Arg	Asn	Arg	Glu	Lys	Leu	Val	Glu		
Phe	Leu	Ser	Glu	Phe	His	Asn	Asp	Arg	Thr	Asp	Asp	Glu	Gln	Phe	Asn		
Asp	Glu	Lys	Ala	Tyr	Leu	Ile	Lys	Gln	Ile	Gln	Glu	Met	Lys	Ser	Ser		
Pro	Lys	Glu	Ala	Lys	Lys	Pro	Lys	Ser	Lys	Glu	Asp	Glu	Asn	Gln	Glu		


```

Pro Ala Gly Pro Ser Glu Gly Pro Ser Thr Ser Gln
625                               630                635

<210> SEQ ID NO 15
<211> LENGTH: 339
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster
<400> SEQUENCE: 15
Met Pro Leu Phe Gly Lys Ser Gln Lys Ser Pro Val Glu Leu Val Lys
1      5      10
Ser Leu Lys Glu Ala Ile Asn Ala Leu Glu Ala Gly Asp Arg Lys Val
20     25     30
Glu Lys Ala Gln Glu Asp Val Ser Lys Asn Leu Val Ser Ile Lys Asn
35     40     45
Met Leu Tyr Gly Ser Ser Asp Ala Glu Pro Pro Ala Asp Tyr Val Val
50     55     60
Ala Gln Leu Ser Gln Glu Leu Tyr Asn Ser Asn Leu Leu Leu Leu
65     70     75     80
Ile Gln Asn Leu His Arg Ile Asp Phe Glu Gly Lys Lys His Val Ala
85     90     95
Leu Ile Phe Asn Asn Val Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
100    105    110
Thr Val Glu Tyr Ile Cys Thr Lys Pro Glu Ile Leu Phe Thr Leu Met
115    120    125
Ala Gly Tyr Glu Asp Ala His Pro Glu Ile Ala Leu Asn Ser Gly Thr
130    135    140
Met Leu Arg Glu Cys Ala Arg Tyr Glu Ala Leu Ala Lys Ile Met Leu
145    150    155    160
His Ser Asp Glu Phe Phe Lys Phe Phe Arg Tyr Val Glu Val Ser Thr
165    170    175
Phe Asp Ile Ala Ser Asp Ala Phe Ser Thr Phe Lys Glu Leu Leu Thr
180    185    190
Arg His Lys Leu Leu Cys Ala Glu Phe Leu Asp Ala Asn Tyr Asp Lys
195    200    205
Phe Phe Ser Gln His Tyr Gln Arg Leu Leu Asn Ser Glu Asn Tyr Val
210    215    220
Thr Arg Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
225    230    235    240
His Asn Phe Thr Val Met Thr Arg Tyr Ile Ser Glu Pro Glu Asn Leu
245    250    255
Lys Leu Met Met Asn Met Leu Lys Glu Lys Ser Arg Asn Ile Gln Phe
260    265    270
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Pro
275    280    285
Lys Pro Ile Leu Asp Ile Leu Leu Arg Asn Gln Thr Lys Leu Val Asp
290    295    300
Phe Leu Thr Asn Phe His Thr Asp Arg Ser Glu Asp Glu Gln Phe Asn
305    310    315    320
Asp Glu Lys Ala Tyr Leu Ile Lys Gln Ile Lys Glu Leu Lys Pro Leu
325    330    335

Pro Glu Ala
<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 16

```

Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr
 20

<210> SEQ ID NO 17
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 17

Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20

<210> SEQ ID NO 18
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 18

Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr
 20

<210> SEQ ID NO 19
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 19

Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr
 20

<210> SEQ ID NO 20
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 20

Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20

<210> SEQ ID NO 21
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 21

Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15

Ser Leu Ala Tyr
20

<210> SEQ ID NO 22

<211> LENGTH: 375

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Pro Leu Leu Phe Gly Lys Ser His Lys Ser Pro Ala Asp Val Val
1 5 10 15

Lys Thr Leu Arg Glu Val Leu Thr Ile Leu Asp Lys Leu Pro Pro Pro
20 25 30

Lys Leu Asp Lys Asp Gly Asn Ile Gln Ser Asp Lys Lys Tyr Asp Lys
35 40 45

Ala Leu Asp Glu Val Ser Lys Asn Val Ala Met Ile Lys Ser Phe Ile
50 55 60

Tyr Gly Asn Asp Ser Ala Glu Pro Ser Ser Glu His Val Val Gln Val
65 70 75 80

Ala Gln Leu Ala Gln Glu Val Tyr Asn Ala Asn Ile Leu Pro Met Leu
85 90 95

Ile Lys Met Leu Pro Lys Phe Glu Phe Glu Cys Lys Lys Asp Val Gly
100 105 110

Gln Ile Phe Asn Asn Leu Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
115 120 125

Thr Val Glu Tyr Leu Gly Ala Arg Pro Glu Ile Leu Ile Gln Leu Val
130 135 140

Gln Gly Tyr Ser Val Pro Asp Ile Ala Leu Thr Cys Gly Leu Met Leu
145 150 155 160

Arg Glu Ser Ile Arg His Asp His Leu Ala Lys Ile Ile Leu Tyr Ser
165 170 175

Asp Val Phe Tyr Thr Phe Phe Leu Tyr Val Gln Ser Glu Val Phe Asp
180 185 190

Ile Ser Ser Asp Ala Phe Ser Thr Phe Lys Glu Leu Thr Thr Arg His
195 200 205

Lys Ala Ile Ile Ala Glu Phe Leu Asp Ser Asn Tyr Asp Thr Phe Phe
 210 215 220

Ala Gln Tyr Gln Asn Leu Leu Asn Ser Lys Asn Tyr Val Thr Arg Arg
 225 230 235 240

Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg His Asn Phe
 245 250 255

Asn Thr Met Thr Lys Tyr Ile Ser Asn Pro Asp Asn Leu Arg Leu Met
 260 265 270

Met Glu Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Tyr Glu Ala Phe
 275 280 285

His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Pro Lys Pro Ile
 290 295 300

Ser Asp Ile Leu Asn Arg Asn Arg Glu Lys Leu Val Glu Phe Leu Ser
 305 310 315 320

Glu Phe His Asn Asp Arg Thr Asp Asp Glu Gln Phe Asn Asp Glu Lys
 325 330 335

Ala Tyr Leu Ile Lys Gln Ile Gln Glu Met Lys Ser Ser Pro Lys Glu
 340 345 350

Ala Lys Lys Pro Lys Ser Lys Glu Asp Glu Asn Gln Glu Pro Ala Gly
 355 360 365

Pro Ser Glu Gly Pro Ser Thr Ser Gln
 370 375

<210> SEQ ID NO 23

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: LKB1 substrate

<400> SEQUENCE: 23

Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr Arg Arg Arg
 20

<210> SEQ ID NO 24

<211> LENGTH: 19

<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 24

Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly Ser
1 5 10 15

Pro Leu Tyr

<210> SEQ ID NO 25
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 25

Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly Ser
1 5 10 15

Pro Leu Tyr Arg Arg Arg
20

<210> SEQ ID NO 26
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 26

Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
1 5 10 15

Ser Pro Leu Tyr
20

<210> SEQ ID NO 27
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 27

Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
1 5 10 15

Ser Pro Leu Tyr Arg Arg Arg
20

<210> SEQ ID NO 28
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 28

Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
1 5 10 15

Ser Pro Pro Tyr
20

<210> SEQ ID NO 29
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:

<223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 29
 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 30
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 30
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr
 20
 <210> SEQ ID NO 31
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 31
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 32
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 32
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr
 20
 <210> SEQ ID NO 33
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 33
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 34
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 34

Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20
 <210> SEQ ID NO 35
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 35
 Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 36
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 36
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15
 Ser Leu Ala Tyr
 20
 <210> SEQ ID NO 37
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 37
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15
 Ser Leu Ala Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 38
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 38
 Met Val Ala Gly Leu Thr Leu Gly Lys Gly Pro Glu Ser Pro Asp Gly
 1 5 10 15
 Asp Val Ser
 <210> SEQ ID NO 39
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 39
 Leu Ser Trp Gly Ala Gly Leu Lys Gly Gln Lys Val Ala Thr Ser Tyr
 1 5 10 15
 Glu Ser Ser Leu
 20
 <210> SEQ ID NO 40
 <211> LENGTH: 21
 <212> TYPE: PRT

<213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 40
 Met Glu Gly Ala Ala Pro Val Ala Gly Asp Arg Pro Asp Leu Gly
 1 5 10 15
 Leu Gly Ala Pro Gly
 20
 <210> SEQ ID NO 41
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 41
 Thr Asp Cys Gln Glu Val Thr Ala Thr Tyr Arg Gln Ala Leu Arg Val
 1 5 10 15
 Cys Ser Lys Leu Thr
 20
 <210> SEQ ID NO 42
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 42
 Met Val Met Ala Asp Gly Pro Arg His Leu Gln Arg Gly Pro Val Arg
 1 5 10 15
 Val Gly Phe Tyr Asp
 20
 <210> SEQ ID NO 43
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 43
 Met Val Ile Met Ser Glu Phe Ser Ala Asp Pro Ala Gly Gln Gly Gln
 1 5 10 15
 Gly Gln Gln Lys
 20
 <210> SEQ ID NO 44
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 44
 Gly Asp Cys Glu Met Glu Asp Leu Met Pro Cys Ser Leu Gly Thr Phe
 1 5 10 15
 Val Leu Val Gln
 20
 <210> SEQ ID NO 45
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 45
 Thr Asp Ile Leu Leu Ser Tyr Lys His Pro Glu Val Ser Phe Ser Met
 1 5 10 15
 Glu Gln Ala Gly Val
 20
 <210> SEQ ID NO 46
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 46
 Ser Gly Thr Ser Ile Ala Phe Lys Asn Ile Ala Ser Lys Ile Ala Asn


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1          5          10          15
Glu Leu Lys Leu
20
<210> SEQ ID NO 47
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 47
Met Ser Ser Arg Thr Val Leu Ala Pro Gly Asn Asp Arg Asn Ser Asp
1          5          10          15
Thr His Gly Thr
20
<210> SEQ ID NO 48
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 48
Met Lys Asp Tyr Asp Glu Leu Leu Lys Tyr Tyr Glu Leu His Glu Thr
1          5          10          15
Ile Gly Thr Gly
20
<210> SEQ ID NO 49
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 49
Cys Thr Ser Pro Pro Asp Ser Phe Leu Asp Asp His His Leu Thr Arg
1          5          10          15
<210> SEQ ID NO 50
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 50
Cys Asp Pro Met Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu
1          5          10
<210> SEQ ID NO 51
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha
<400> SEQUENCE: 51
Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Phe
1          5          10
<210> SEQ ID NO 52
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, last residue
mutated to Ala
<400> SEQUENCE: 52
Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Ala
1          5          10
<210> SEQ ID NO 53
<211> LENGTH: 12
<212> TYPE: PRT

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<213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, third last residue mutated t
 o Ala
 <400> SEQUENCE: 53
 Asn Leu Glu Glu Leu Glu Val Asp Asp Ala Glu Phe
 1 5 10
 <210> SEQ ID NO 54
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, second last residue mutated t
 o Ala
 <400> SEQUENCE: 54
 Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Ala Phe
 1 5 10
 <210> SEQ ID NO 55
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 6 residues STRAD alpha
 <400> SEQUENCE: 55
 Val Asp Asp Trp Glu Phe
 1 5
 <210> SEQ ID NO 56
 <211> LENGTH: 547
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 56
 Met Ala Glu Pro Ser Gly Ser Pro Val His Val Gln Leu Pro Gln Gln
 1 5 10 15
 Ala Ala Pro Val Thr Ala Ala Ala Ala Ala Pro Ala Ala Ala Thr
 20 25 30
 Ala Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Pro Ala
 35 40 45
 Pro Ala Pro Ala Ala Gln Ala Val Gly Trp Pro Ile Cys Arg Asp Ala
 50 55 60
 Tyr Glu Leu Gln Glu Val Ile Gly Ser Gly Ala Thr Ala Val Val Gln
 65 70 75 80
 Ala Ala Leu Cys Lys Pro Arg Gln Glu Arg Val Ala Ile Lys Arg Ile
 85 90 95
 Asn Leu Glu Lys Cys Gln Thr Ser Met Asp Glu Leu Leu Lys Glu Ile
 100 105 110
 Gln Ala Met Ser Gln Cys Ser His Pro Asn Val Val Thr Tyr Tyr Thr
 115 120 125
 Ser Phe Val Val Lys Asp Glu Leu Trp Leu Val Met Lys Leu Leu Ser
 130 135 140
 Gly Gly Ser Met Leu Asp Ile Ile Lys Tyr Ile Val Asn Arg Gly Glu
 145 150 155 160
 His Lys Asn Gly Val Leu Glu Glu Ala Ile Ile Ala Thr Ile Leu Lys
 165 170 175
 Glu Val Leu Glu Gly Leu Asp Tyr Leu His Arg Asn Gly Gln Ile His
 180 185 190

Arg Asp Leu Lys Ala Gly Asn Ile Leu Leu Gly Glu Asp Gly Ser Val
 195 200 205
 Gln Ile Ala Asp Phe Gly Val Ser Ala Phe Leu Ala Thr Gly Gly Asp
 210 215 220
 Val Thr Arg Asn Lys Val Arg Lys Thr Phe Val Gly Thr Pro Cys Trp
 225 230 235 240
 Met Ala Pro Glu Val Met Glu Gln Val Arg Gly Tyr Asp Phe Lys Ala
 245 250 255
 Asp Met Trp Ser Phe Gly Ile Thr Ala Ile Glu Leu Ala Thr Gly Ala
 260 265 270
 Ala Pro Tyr His Lys Tyr Pro Pro Met Lys Val Leu Met Leu Thr Leu
 275 280 285
 Gln Asn Asp Pro Pro Thr Leu Glu Thr Gly Val Glu Asp Lys Glu Met
 290 295 300
 Met Lys Lys Tyr Gly Lys Ser Phe Arg Lys Leu Leu Ser Leu Cys Leu
 305 310 315 320
 Gln Lys Asp Pro Ser Lys Arg Pro Thr Ala Ala Glu Leu Leu Lys Cys
 325 330 335
 Lys Phe Phe Gln Lys Ala Lys Asn Arg Glu Tyr Leu Ile Glu Lys Leu
 340 345 350
 Leu Thr Arg Thr Pro Asp Ile Ala Gln Arg Ala Lys Lys Val Arg Arg
 355 360 365
 Val Pro Gly Ser Ser Gly His Leu His Lys Thr Glu Asp Gly Asp Trp
 370 375 380
 Glu Trp Ser Asp Asp Glu Met Asp Glu Lys Ser Glu Glu Gly Lys Ala
 385 390 395 400
 Ala Phe Ser Gln Glu Lys Ser Arg Arg Val Lys Glu Glu Asn Pro Glu
 405 410 415
 Ile Ala Val Ser Ala Ser Thr Ile Pro Glu Gln Ile Gln Ser Leu Ser
 420 425 430
 Val His Asp Ser Gln Gly Pro Pro Asn Ala Asn Glu Asp Tyr Arg Glu
 435 440 445
 Ala Ser Ser Cys Ala Val Asn Leu Val Leu Arg Leu Arg Asn Ser Arg
 450 455 460
 Lys Glu Leu Asn Asp Ile Arg Phe Glu Phe Thr Pro Gly Arg Asp Thr
 465 470 475 480
 Ala Asp Gly Val Ser Gln Glu Leu Phe Ser Ala Gly Leu Val Asp Gly
 485 490 495
 His Asp Val Val Ile Val Ala Ala Asn Leu Gln Lys Ile Val Asp Asp
 500 505 510
 Pro Lys Ala Leu Lys Thr Leu Thr Phe Lys Leu Ala Ser Gly Cys Asp
 515 520 525
 Gly Ser Glu Ile Pro Asp Glu Val Lys Leu Ile Gly Phe Ala Gln Leu
 530 535 540
 Ser Val Ser
 545

<210> SEQ ID NO 57

<211> LENGTH: 527

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

Met Ser Glu Asp Ser Ser Ala Leu Pro Trp Ser Ile Asn Arg Asp Asp
 1 5 10 15
 Tyr Glu Leu Gln Glu Val Ile Gly Ser Gly Ala Thr Ala Val Val Gln
 20 25 30
 Ala Ala Tyr Cys Ala Pro Lys Lys Glu Lys Val Ala Ile Lys Arg Ile
 35 40 45

Asn Leu Glu Lys Cys Gln Thr Ser Met Asp Glu Leu Leu Lys Glu Ile
 50 55 60
 Gln Ala Met Ser Gln Cys His His Pro Asn Ile Val Ser Tyr Tyr Thr
 65 70 75 80
 Ser Phe Val Val Lys Asp Glu Leu Trp Leu Val Met Lys Leu Leu Ser
 85 90 95
 Gly Gly Ser Val Leu Asp Ile Ile Lys His Ile Val Ala Lys Gly Glu
 100 105 110
 His Lys Ser Gly Val Leu Asp Glu Ser Thr Ile Ala Thr Ile Leu Arg
 115 120 125
 Glu Val Leu Glu Gly Leu Glu Tyr Leu His Lys Asn Gly Gln Ile His
 130 135 140
 Arg Asp Val Lys Ala Gly Asn Ile Leu Leu Gly Glu Asp Gly Ser Val
 145 150 155 160
 Gln Ile Ala Asp Phe Gly Val Ser Ala Phe Leu Ala Thr Gly Gly Asp
 165 170 175
 Ile Thr Arg Asn Lys Val Arg Lys Thr Phe Val Gly Thr Pro Cys Trp
 180 185 190
 Met Ala Pro Glu Val Met Glu Gln Val Arg Gly Tyr Asp Phe Lys Ala
 195 200 205
 Asp Ile Trp Ser Phe Gly Ile Thr Ala Ile Glu Leu Ala Thr Gly Ala
 210 215 220
 Ala Pro Tyr His Lys Tyr Pro Pro Met Lys Val Leu Met Leu Thr Leu
 225 230 235 240
 Gln Asn Asp Pro Pro Ser Leu Glu Thr Gly Val Gln Asp Lys Glu Met
 245 250 255
 Leu Lys Lys Tyr Gly Lys Ser Phe Arg Lys Met Ile Ser Leu Cys Leu
 260 265 270
 Gln Lys Asp Pro Glu Lys Arg Pro Thr Ala Ala Glu Leu Leu Arg His
 275 280 285
 Lys Phe Phe Gln Lys Ala Lys Asn Lys Glu Phe Leu Gln Glu Lys Thr
 290 295 300
 Leu Gln Arg Ala Pro Thr Ile Ser Glu Arg Ala Lys Lys Val Arg Arg
 305 310 315 320
 Val Pro Gly Ser Ser Gly Arg Leu His Lys Thr Glu Asp Gly Gly Trp
 325 330 335
 Glu Trp Ser Asp Asp Glu Phe Asp Glu Glu Ser Glu Glu Gly Lys Ala
 340 345 350
 Ala Ile Ser Gln Leu Arg Ser Pro Arg Val Lys Glu Ser Ile Ser Asn
 355 360 365
 Ser Glu Leu Phe Pro Thr Thr Asp Pro Val Gly Thr Leu Leu Gln Val
 370 375 380
 Pro Glu Gln Ile Ser Ala His Leu Pro Gln Pro Ala Gly Gln Ile Ala
 385 390 395 400
 Thr Gln Pro Thr Gln Val Ser Leu Pro Pro Thr Ala Glu Pro Ala Lys
 405 410 415
 Thr Ala Gln Ala Leu Ser Ser Gly Ser Gly Ser Gln Glu Thr Lys Ile
 420 425 430
 Pro Ile Ser Leu Val Leu Arg Leu Arg Asn Ser Lys Lys Glu Leu Asn
 435 440 445
 Asp Ile Arg Phe Glu Phe Thr Pro Gly Arg Asp Thr Ala Glu Gly Val
 450 455 460
 Ser Gln Glu Leu Ile Ser Ala Gly Leu Val Asp Gly Arg Asp Leu Val
 465 470 475 480
 Ile Val Ala Ala Asn Leu Gln Lys Ile Val Glu Glu Pro Gln Ser Asn
 485 490 495
 Arg Ser Val Thr Phe Lys Leu Ala Ser Gly Val Glu Gly Ser Asp Ile

500
 Pro Asp Asp Gly Lys Leu Ile Gly Phe Ala Gln Leu Ser Ile Ser
 515 520 525

<210> SEQ ID NO 58
 <211> LENGTH: 560
 <212> TYPE: PRT
 <213> ORGANISM: *Saccharomyces cerevisiae*
 <400> SEQUENCE: 58

Met Val Leu Leu Lys Glu Pro Val Gln Pro Leu Pro Arg Ser Ser Leu
 1 5 10 15
 Leu Tyr Asn Asn Ala Ser Asn Ser Ser Ser Arg Ile Lys Glu Thr Arg
 20 25 30
 Lys Val Lys Leu Leu Tyr Asn Pro Leu Thr Lys Arg Gln Ile Leu Asn
 35 40 45
 Asn Phe Glu Ile Leu Ala Thr Leu Gly Asn Gly Gln Tyr Gly Lys Val
 50 55 60
 Lys Leu Ala Arg Asp Leu Gly Thr Gly Ala Leu Val Ala Ile Lys Ile
 65 70 75 80
 Leu Asn Arg Phe Glu Lys Arg Ser Gly Tyr Ser Leu Gln Leu Lys Val
 85 90 95
 Glu Asn Pro Arg Val Asn Gln Glu Ile Glu Val Met Lys Arg Cys His
 100 105 110
 His Glu Asn Val Val Glu Leu Tyr Glu Ile Leu Asn Asp Pro Glu Ser
 115 120 125
 Thr Lys Val Tyr Leu Val Leu Glu Tyr Cys Ser Arg Gly Pro Val Lys
 130 135 140
 Trp Cys Pro Glu Asn Lys Met Glu Ile Lys Ala Val Gly Pro Ser Ile
 145 150 155 160
 Leu Thr Phe Gln Gln Ser Arg Lys Val Val Leu Asp Val Val Ser Gly
 165 170 175
 Leu Glu Tyr Leu His Ser Gln Gly Ile Thr His Arg Asp Ile Lys Pro
 180 185 190
 Ser Asn Leu Leu Ile Ser Ser Asn Gly Thr Val Lys Ile Ser Asp Phe
 195 200 205
 Gly Val Ala Met Ser Thr Ala Thr Gly Ser Thr Asn Ile Gln Ser Ser
 210 215 220
 His Glu Gln Leu Leu Lys Ser Arg Ala Leu Gly Thr Pro Ala Phe Phe
 225 230 235 240
 Ala Pro Glu Leu Cys Ser Thr Glu Lys Glu Tyr Ser Cys Ser Ser Ala
 245 250 255
 Ile Asp Ile Trp Ser Leu Gly Val Thr Ile Tyr Cys Leu Leu Phe Gly
 260 265 270
 Lys Leu Pro Phe Asn Ala Asn Ser Gly Leu Glu Leu Phe Asp Ser Ile
 275 280 285
 Ile Asn Lys Pro Leu Glu Phe Pro Ser Tyr Glu Glu Met Leu Asn Gly
 290 295 300
 Ala Thr Ser Gly Ile Thr Met Glu Glu Tyr Thr Asp Ala Lys Asp Leu
 305 310 315 320
 Leu Lys Lys Leu Leu Gln Lys Asp Pro Asp Lys Arg Ile Lys Leu Ala
 325 330 335
 Asp Ile Lys Val His Pro Phe Met Cys His Tyr Gly Lys Ser Asp Ala
 340 345 350
 Ala Ser Val Leu Thr Asn Leu Glu Thr Phe His Glu Leu Lys Val Ser
 355 360 365
 Pro Pro Ser Ser Cys Lys Arg Val Glu Leu Val Ser Leu Pro Val Asn
 370 375 380
 Ser Ser Phe Ala Ser Leu Asp Ser Val Tyr Met Glu Asn Phe Asp His

385		390		395		400
Asn Asn Leu Arg Thr Gly Ala Asp Arg Asn Ser Thr Tyr Ser Pro Ser						
	405			410		415
Ile Tyr Asp Ala Asn Thr Leu Ser Pro Ser Ala Tyr His Asn Ile Gly						
	420		425		430	
Ser Arg Glu Ser Ser Tyr Ser Ser Phe Ser Ser Phe Thr Ser Ser Thr		440		445		
	435					
Ala Phe Ala Ser Gln Ile Ser Ile Gln Asp Ala Pro Ala Ile Gly Asp				460		
	450	455				
Gln Gln Cys Leu Ile Gly Glu Ser Gly Ser Ser Leu Arg Val Asn Ser				475		480
465	470					
Cys Glu Phe Pro Gln Tyr Thr Thr Met Ser Pro Val Gly Glu Tyr Pro			490		495	
	485					
Phe Glu Ser Thr Glu Ala Ser Leu Ser Ser Thr Leu Thr Pro Val Gly		505		510		
	500					
Asn Val Pro Gln Arg Ile Lys Ala His Leu Val Glu Gly Lys Ser Asn						
	515	520		525		
Ser Lys Asp Asp Leu Arg Ile Glu Ala Asp Ala Ser Leu Val Phe Glu						
	530	535		540		
Ala Ser Asp Ala Gln Arg Thr Arg Arg Arg Met Ser Leu Tyr Lys Leu						
545	550		555		560	

<210> SEQ ID NO 59

<211> LENGTH: 1142

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 59

Met Asp Arg Ser Asp Lys Lys Val Asn Val Glu Glu Val Asn Val Pro						
1	5	10	15			
Ser Asn Leu Gln Ile Glu Leu Glu Lys Ser Gly Thr Ser Ser Ser Val						
	20	25	30			
Ser Leu Arg Ser Pro Thr Lys Ser Ser Ala Thr Asn Leu Ala Gly Met		40	45			
	35					
Ala Glu Gly Ala Arg Asp Asn Ala Ser Ile Ala Ser Ser Val Asp						
	50	55	60			
Ser Leu Asn Met Leu Leu Glu Arg Gln Arg Val Arg Gln Leu Asn His						
65	70	75				80
Pro Gln His Gln Gln His Ile Ser Ser Ser Leu Ala Lys Thr Pro Thr						
	85	90				95
Thr Thr Ser Ser Phe Cys Ser Ser Gly Ser Ser Lys Asn Lys Val Lys						
	100	105	110			
Glu Thr Asn Arg Ile Ser Leu Thr Tyr Asp Pro Val Ser Lys Arg Lys						
	115	120	125			
Val Leu Asn Thr Tyr Glu Ile Ile Lys Glu Leu Gly His Gly Gln His						
	130	135	140			
Gly Lys Val Lys Leu Ala Arg Asp Ile Leu Ser Lys Gln Leu Val Ala						
145	150	155				160
Ile Lys Ile Val Asp Arg His Glu Lys Lys Gln Arg Lys Phe Phe Thr						
	165	170				175
Phe Ile Lys Ser Ser Lys Ile Ser Glu Asn Asp Lys Ile Lys Arg Glu						
	180	185				190
Ile Ala Ile Met Lys Lys Cys His His Lys His Val Val Gln Leu Ile						
	195	200				205
Glu Val Leu Asp Asp Leu Lys Ser Arg Lys Ile Tyr Leu Val Leu Glu						
	210	215	220			
Tyr Cys Ser Arg Gly Glu Val Lys Trp Cys Pro Pro Asp Cys Met Glu						
225	230		235			240
Ser Asp Ala Lys Gly Pro Ser Leu Leu Ser Phe Gln Glu Thr Arg Glu						

					245					250							255
Ile	Leu	Arg	Gly	Val	Val	Leu	Gly	Leu	Glu	Tyr	Leu	His	Tyr	Gln	Gly		
			260					265					270				
Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ala	Asn	Leu	Leu	Ile	Ser	Gly	Asp		
		275					280					285					
Gly	Thr	Val	Lys	Ile	Ser	Asp	Phe	Gly	Val	Ser	Leu	Ala	Ala	Ser	Ser		
		290				295					300						
Thr	Asn	Ser	Ser	Asp	Ser	Ser	Glu	Ser	Leu	Asp	Glu	Leu	Glu	Leu	Ala		
305					310					315					320		
Lys	Thr	Val	Gly	Thr	Pro	Ala	Phe	Phe	Ala	Pro	Glu	Met	Cys	Leu	Gly		
				325					330					335			
Glu	Asp	Ala	Phe	Thr	Arg	Tyr	Asn	Leu	Thr	Lys	Glu	Asn	Leu	Phe	Arg		
		340						345					350				
Gly	Ser	Cys	Ile	Ser	Phe	Met	Ile	Asp	Ile	Trp	Ala	Val	Gly	Val	Thr		
		355					360					365					
Leu	Tyr	Cys	Leu	Leu	Phe	Gly	Met	Leu	Pro	Phe	Phe	Ser	Asp	Phe	Glu		
		370				375					380						
Leu	Lys	Leu	Phe	Glu	Lys	Ile	Val	Asn	Asp	Pro	Leu	Lys	Phe	Pro	Thr		
385					390					395					400		
Phe	Lys	Glu	Ile	Gln	Ser	Asn	Lys	Val	Ser	Lys	Val	Ser	Cys	Glu	Glu		
				405					410					415			
Glu	Tyr	Glu	Met	Ala	Lys	Asp	Leu	Leu	Lys	Leu	Leu	Glu	Lys	Asn			
		420					425					430					
Pro	Gln	Lys	Arg	Met	Thr	Ile	Pro	Ala	Ile	Lys	Lys	His	Pro	Phe	Val		
		435					440					445					
Ser	Trp	Asp	Phe	Asp	His	Val	Pro	Glu	Asn	Asp	Glu	Lys	Leu	Leu	Ser		
		450				455					460						
Ser	Val	Leu	Glu	Gln	Lys	Leu	Arg	Phe	Gln	Cys	Asn	Gln	Thr	Asp	Gln		
465					470					475					480		
Phe	Glu	Pro	Ile	Ser	Ile	Ser	Lys	His	Glu	Leu	Lys	Asn	Ala	Val	Ser		
				485					490					495			
Gly	Val	Gly	Lys	Lys	Ile	Lys	Glu	Ser	Val	Leu	Lys	Ser	Ile	Pro	Leu		
			500				505						510				
Lys	Asp	Pro	Ser	Asp	Leu	Ser	Asn	Lys	Asn	Tyr	Leu	His	Pro	Thr	Glu		
		515					520					525					
Thr	Thr	Arg	Gly	Arg	Gly	Asp	Ala	Asn	Val	Ile	Val	Ser	Glu	Gly	Ser		
		530				535					540						
Val	Leu	Ser	Asn	Ile	Lys	Glu	Leu	Ser	Ala	Asn	Asp	Gly	Cys	Leu	Asn		
545					550					555					560		
Thr	Asp	Ser	Asp	Thr	Asn	Ile	Asn	Ile	Asn	Asp	Asp	Asp	His	Tyr	Ser		
				565					570								

Thr	Ser	Tyr	Asn	Ser	Gly	Arg	Pro	Ser	Ser	Arg	Thr	Gly	Arg	Met	Asn	705	710	715	720
Ser	Arg	Asn	Gln	Asn	Leu	Pro	Lys	Ile	Pro	Asn	Ser	Leu	Ser	Lys	Ile	725	730	735	740
Ser	Thr	Thr	Lys	Leu	Thr	Glu	Leu	Arg	Val	Pro	Lys	Asp	Ser	Glu	Ile	740	745	750	755
Pro	Ser	Pro	Ala	Lys	Asn	Pro	Asn	Ala	Asp	Arg	Leu	Arg	Arg	Phe	Pro	760	765	770	775
Val	Lys	Lys	Asn	Thr	Lys	Thr	Pro	Ala	Ile	Lys	Asp	Pro	Pro	Arg	Ile	780	785	790	795
Asn	Ile	Asn	Ser	Ser	Asp	Lys	Ser	Gly	Ser	Lys	Asn	Ser	Pro	Ile	Lys	800	805	810	815
Ser	Leu	Tyr	Gln	Arg	Met	Lys	Gln	Ser	Lys	Asp	Asn	Ser	Lys	Thr	Phe	820	825	830	835
Glu	Val	Arg	Arg	Gly	Asn	Phe	Phe	Ser	His	Phe	Asn	Gly	Asp	Asp	Asp	840	845	850	855
Asp	Ser	Ser	Ser	Gln	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ser	Glu	Ser	Asp	860	865	870	875
Ser	Glu	Leu	Ser	Ser	Thr	Ser	Ser	Ser	Cys	Thr	Ser	Gly	Thr	Gln	Ser	880	885	890	895
Arg	Asn	Ser	Ser	Asn	Asn	Asn	Ala	Tyr	Ser	Glu	Thr	Glu	Ser	Leu	Pro	900	905	910	915
Arg	Asn	Ser	Ser	Asn	Asn	Asn	Ala	Tyr	Ser	Glu	Thr	Glu	Ser	Leu	Pro	920	925	930	935
Phe	Glu	Phe	Gly	Val	Asp	Ser	Glu	Asp	Gly	Ser	Gly	Val	Leu	Leu	Arg	940	945	950	955
Asp	Leu	Pro	Asn	Glu	Asp	Gln	Ile	Arg	Pro	Phe	Leu	Asp	Ile	Gln	Pro	960	965	970	975
Cys	Arg	Arg	Met	Lys	Val	Lys	Ser	Ser	Leu	Asn	Leu	Glu	Pro	Pro	Ser	980	985	990	995
Val	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Glu	Asp	Glu	Leu	Ile	Leu	1000	1005	1010	1015
Asn	Val	Gly	Thr	Ala	Gly	His	Arg	Arg	Arg	His	Asn	Ser	Ser	Lys	Leu	1020	1025	1030	1035
Asn	Gly	Asn	Asn	Asp	His	Arg	Lys	Asp	Lys	Asn	Phe	Asp	Lys	Val		1040	1045	1050	1055
Leu	Tyr	Ser	Arg	Asp	Leu	Leu	Lys	Asp	Ala	Leu	Ser	Ser	Thr	Asn		1060	1065	1070	1075
Ala	Gly	Arg	Arg	Arg	Ser	Ile	Pro	Ser	Asn	Lys	Ile	Arg	Gly	Arg		1080	1085	1090	1095
Lys	Asp	Ala	Ser	Ile	Thr	Met	Ser	Thr	Asn	Val	Gly	Asn	Asp	Glu		1100	1105	1110	1115
His	Ala	Arg	Asn	Thr	Ser	Cys	His	Gly	Asp	Lys	Gly	Gln	Glu	Asn		1120	1125	1130	1135
Gly	Ala	Ile	Lys	Gln	Arg	Thr	His	Glu	Arg	Ser	Arg	Ser	Leu	Thr		1140	1145	1150	1155
Val	Ala	Glu	Leu	Asn	Glu	Glu	Lys	Arg	Arg	Ser	Ala	Leu	Pro			1160	1165	1170	1175

<211> LENGTH: 640

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 60

```
Met Ser Pro Arg Gln Leu Ile Pro Thr Leu Ile Pro Glu Trp Ala Pro
1      5      10      15
Leu Ser Gln Gln Ser Cys Ile Arg Glu Asp Glu Leu Asp Ser Pro Pro
20      25      30
Ile Thr Pro Thr Ser Gln Thr Ser Ser Phe Gly Ser Ser Phe Ser Gln
35      40      45
Gln Lys Pro Thr Tyr Ser Thr Ile Ile Gly Glu Asn Ile His Thr Ile
50      55      60
Leu Asp Glu Ile Arg Pro Tyr Val Lys Lys Ile Thr Val Ser Asp Gln
65      70      75      80
Asp Lys Lys Thr Ile Asn Gln Tyr Thr Leu Gly Val Ser Ala Gly Ser
85      90      95
Gly Gln Phe Gly Tyr Val Arg Lys Ala Tyr Ser Ser Thr Leu Gly Lys
100      105      110
Val Val Ala Val Lys Ile Ile Pro Lys Lys Pro Trp Asn Ala Gln Gln
115      120      125
Tyr Ser Val Asn Gln Val Met Arg Gln Ile Gln Leu Trp Lys Ser Lys
130      135      140
Gly Lys Ile Thr Thr Asn Met Ser Gly Asn Glu Ala Met Arg Leu Met
145      150      155      160
Asn Ile Glu Lys Cys Arg Trp Glu Ile Phe Ala Ala Ser Arg Leu Arg
165      170      175
Asn Asn Val His Ile Val Arg Leu Ile Glu Cys Leu Asp Ser Pro Phe
180      185      190
Ser Glu Ser Ile Trp Ile Val Thr Asn Trp Cys Ser Leu Gly Glu Leu
195      200      205
Gln Trp Lys Arg Asp Asp Asp Glu Asp Ile Leu Pro Gln Trp Lys Lys
210      215      220
Ile Val Ile Ser Asn Cys Ser Val Ser Thr Phe Ala Lys Lys Ile Leu
225      230      235      240
Glu Asp Met Thr Lys Gly Leu Glu Tyr Leu His Ser Gln Gly Cys Ile
245      250      255
His Arg Asp Ile Lys Pro Ser Asn Ile Leu Leu Asp Glu Glu Glu Lys
260      265      270
Val Ala Lys Leu Ser Asp Phe Gly Ser Cys Ile Phe Thr Pro Gln Ser
275      280      285
Leu Pro Phe Ser Asp Ala Asn Phe Glu Asp Cys Phe Gln Arg Glu Leu
290      295      300
Asn Lys Ile Val Gly Thr Pro Ala Phe Ile Ala Pro Glu Leu Cys His
305      310      315      320
Leu Gly Asn Ser Lys Arg Asp Phe Val Thr Asp Gly Phe Lys Leu Asp
325      330      335
Ile Trp Ser Leu Gly Val Thr Leu Tyr Cys Leu Leu Tyr Asn Glu Leu
340      345      350
Pro Phe Phe Gly Glu Asn Glu Phe Glu Thr Tyr His Lys Ile Ile Glu
355      360      365
Val Ser Leu Ser Ser Lys Ile Asn Gly Asn Thr Leu Asn Asp Leu Val
370      375      380
Ile Lys Arg Leu Leu Glu Lys Asp Val Thr Leu Arg Ile Ser Ile Gln
385      390      395      400
Asp Leu Val Lys Val Leu Ser Arg Asp Gln Pro Ile Asp Ser Arg Asn
405      410      415
His Ser Gln Ile Ser Ser Ser Ser Val Asn Pro Val Arg Asn Glu Gly
```

420										425										430									
Pro	Val	Arg	Arg	Phe	Phe	Gly	Arg	Leu	Leu	Thr	Lys	Lys	Gly	Lys	Lys														
				435				440					445																
Lys	Thr	Ser	Gly	Lys	Gly	Lys	Asp	Lys	Val	Leu	Val	Ser	Ala	Thr	Ser														
			450				455					460																	
Lys	Val	Thr	Pro	Ser	Ile	His	Ile	Asp	Glu	Glu	Pro	Asp	Lys	Glu	Cys														
465					470					475					480														
Phe	Ser	Thr	Thr	Val	Leu	Arg	Ser	Ser	Pro	Asp	Ser	Ser	Asp	Tyr	Cys														
				485						490					495														
Ser	Ser	Leu	Gly	Glu	Glu	Ala	Ile	Gln	Val	Thr	Asp	Phe	Leu	Asp	Thr														
			500						505					510															
Phe	Cys	Arg	Ser	Asn	Glu	Ser	Leu	Pro	Asn	Leu	Thr	Val	Asn	Asn	Asp														
			515				520					525																	
Lys	Gln	Asn	Ser	Asp	Met	Lys	Thr	Asp	Arg	Ser	Glu	Ser	Ser	Ser	His														
			530			535					540																		
Ser	Ser	Leu	Lys	Ile	Pro	Thr	Pro	Ile	Lys	Ala	Met	Ile	Arg	Leu	Lys														
545					550					555				560															
Ser	Ser	Pro	Lys	Glu	Asn	Gly	Asn	Arg	Thr	His	Ile	Asn	Cys	Ser	Gln														
				565					570					575															
Asp	Lys	Pro	Ser	Ser	Pro	Leu	Met	Asp	Arg	Thr	Val	Gly	Lys	Arg	Thr														
				580				585						590															
Val	Asn	Asn	Ser	Gly	Ala	Arg	Lys	Leu	Ala	His	Ser	Ser	Asn	Ile	Leu														
			595				600					605																	
Asn	Phe	Lys	Ala	Tyr	Ile	Asn	Ser	Glu	Asp	Ser	Asp	Ile	Arg	Glu	Thr														
			610			615					620																		
Val	Glu	Asp	Val	Lys	Thr	Tyr	Leu	Asn	Phe	Ala	Asp	Asn	Gly	Gln	Ile														
625					630					635				640															

	195		200		205				
Arg	Arg	Pro	Pro	Pro	Arg	Gly	Thr	Arg	Pro
	210					215			220
Gln	Pro	Arg	Gly	Pro	Ile	Glu	Gln	Val	Tyr
	225				230				235
Lys	Lys	Leu	Asp	His	Pro	Asn	Val	Val	Lys
			245					250	
Asp	Pro	Asn	Glu	Asp	His	Leu	Tyr	Met	Val
			260					265	
Gly	Pro	Val	Met	Glu	Val	Pro	Thr	Leu	Lys
		275					280		
Ala	Arg	Phe	Tyr	Phe	Gln	Asp	Leu	Ile	Lys
	290					295			
Tyr	Gln	Lys	Ile	Ile	His	Arg	Asp	Ile	Lys
	305				310				315
Gly	Glu	Asp	Gly	His	Ile	Lys	Ile	Ala	Asp
			325					330	
Phe	Lys	Gly	Ser	Asp	Ala	Leu	Leu	Ser	Asn
			340					345	
Phe	Met	Ala	Pro	Glu	Ser	Leu	Ser	Glu	Thr
		355				360			
Lys	Ala	Leu	Asp	Val	Trp	Ala	Met	Gly	Val
	370					375			
Phe	Gly	Gln	Cys	Pro	Phe	Met	Asp	Glu	Arg
	385				390				395
Lys	Ile	Lys	Ser	Gln	Ala	Leu	Glu	Phe	Pro
			405					410	
Glu	Asp	Leu	Lys	Asp	Leu	Ile	Thr	Arg	Met
			420					425	
Ser	Arg	Ile	Val	Val	Pro	Glu	Ile	Lys	Ile
		435						440	
Arg	Lys	Arg	Ser	Phe	Gly	Asn	Pro	Phe	Glu
	450					455			
Arg	Ser	Leu	Ser	Ala	Pro	Gly	Asn	Leu	Leu
	465				470				475
Glu	Cys	Glu	Ser	Leu	Ser	Glu	Leu	Lys	Glu
			485					490	
Pro	Pro	Gly	His	Arg	Pro	Ala	Pro	Arg	Gly
		500						505	
Val	Arg	Gly	Ser	Pro	Cys	Val	Glu	Ser	Cys
		515						520	
Ser	Pro	Ala	Arg	Met	His	Pro	Leu	Arg	Pro
	530					535			540

Glu
545

<210> SEQ ID NO 62

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Consensus for figure 12

<400> SEQUENCE: 62

Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ile	Lys	Thr	Val	Leu	Tyr	Pro	Leu
1		5						10					15	
Thr	Lys	Arg	Gln	Ile	Leu	Asn	Asn	Tyr	Ile	Leu	Gly	Gly	Gln	Tyr
		20						25				30		
Lys	Val	Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Ile	Lys	Ile	Leu	Lys

35	40	45
Lys Lys Tyr Lys Asp Arg Val Lys Glu Ile Val Met Lys Arg Leu His		
50	55	60
His Asn Val Val Leu Ile Glu Val Leu Asp Asp Pro Ser Lys Val Tyr		
65	70	75
Leu Val Leu Glu Tyr Cys Ser Gly Val Trp Cys Met Glu Ile Val Pro		
85	90	95
Ile Leu Ser Gln Ala Arg Val Val Asp Val Val Gly Leu Glu Tyr Leu		
100	105	110
His Ser Gln Gly Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Leu		
115	120	125
Ile Ser Asp Gly Thr Val Lys Ile Ser Asp Phe Gly Val Thr Ser Asp		
130	135	140
Ser Leu Arg Val Gly Thr Pro Ala Phe Ala Pro Glu Leu Cys Tyr Phe		
145	150	155
Ile Asp Ile Trp Ser Leu Gly Val Thr Leu Tyr Cys Leu Leu Phe Gly		
165	170	175
Leu Pro Phe Ala Asp Leu Leu Phe Asp Lys Ile Ile Leu Phe Pro Glu		
180	185	190
Met Glu Glu Leu Lys Asp Leu Leu Lys Lys Leu Leu Glu Asn Lys Asn		
195	200	205
Pro Lys Arg Ile Leu Ile Lys His Pro Phe Val Asp His Pro Asp Val		
210	215	220
Leu Thr Glu Leu Lys Pro Leu Arg Val Glu Pro Val Ser Leu Lys Ser		
225	230	235
Ser Leu Gly		
		240

<210> SEQ ID NO 63

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

Asp Phe Gly Phe Ala Lys Arg Val Lys Gly Arg Thr Trp Thr Leu Cys	
1	15
Gly Thr Pro Glu Tyr Leu Ala Pro Glu	
20	25

<210> SEQ ID NO 64

<211> LENGTH: 28

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg	
1	15
Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu	
20	25

<210> SEQ ID NO 65

<211> LENGTH: 27

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

Asp Phe Gly Leu Ser Asn Leu Tyr Gln Lys Asp Lys Phe Leu Gln Thr	
1	15
Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu	
20	25

<210> SEQ ID NO 66

<211> LENGTH: 26

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66
 Asp Phe Gly Leu Ser Asn Tyr His Gln Gly Lys Phe Leu Gln Thr Phe
 1 5 10 15
 Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu
 20 25

<210> SEQ ID NO 67
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 67
 Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr
 1 5 10 15
 Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu
 20 25

<210> SEQ ID NO 68
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 68
 Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr
 1 5 10 15
 Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu
 20 25

<210> SEQ ID NO 69
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 69
 Asp Phe Gly Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr
 1 5 10 15
 Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 70
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 70
 Asp Phe Gly Phe Gly Asn Phe Phe Lys Ser Gly Glu Leu Leu Ala Thr
 1 5 10 15
 Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 71
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana
 <400> SEQUENCE: 71
 Asp Phe Gly Leu Ser Asn Ile Met Arg Asp Gly His Phe Leu Lys Thr
 1 5 10 15
 Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 72
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana
 <400> SEQUENCE: 72
 Asp Phe Gly Leu Ser Asn Val Met Arg Asp Gly His Phe Leu Lys Thr
 1 5 10 15

Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 73
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 73
Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr
1 5 10 15
Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 74
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 74
Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr
1 5 10 15
Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 75
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 75
Asp Phe Gly Leu Ser Asn Ile Met Thr Asp Gly Asn Phe Leu Lys Thr
1 5 10 15
Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 76
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 76
Asp Phe Gly Phe Ser Asn Leu Phe Thr Pro Gly Gln Leu Leu Lys Thr
1 5 10 15
Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 77
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 77
Asp Phe Gly Leu Cys Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu
1 5 10 15
Gln Thr Cys Cys Gly Ser Leu Ala Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 78
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: consensus from figure 19
<400> SEQUENCE: 78
Asp Phe Gly Leu Ser Asn Leu Gly Phe Leu Thr Ser Cys Gly Ser Pro
1 5 10 15
Tyr Ala Ala Pro Glu

20

<210> SEQ ID NO 79
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 79
 Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr
 1 5 10 15
 Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 80
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 80
 Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr
 1 5 10 15
 Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 81
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 81
 Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr
 1 5 10 15
 Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 82
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 82
 Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser Lys Leu Asp Thr
 1 5 10 15
 Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 83
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 83
 Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr Arg Arg Arg
 20

<210> SEQ ID NO 84
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 84
 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20

<210> SEQ ID NO 85
 <211> LENGTH: 23

<212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 85
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr Arg Arg Arg
 20

<210> SEQ ID NO 86
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 86
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr Arg Arg Arg
 20

<210> SEQ ID NO 87
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 87
 Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20

<210> SEQ ID NO 88
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 88
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15
 Ser Leu Ala Tyr Arg Arg Arg
 20

<210> SEQ ID NO 89
 <211> LENGTH: 32
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 89
 Ile Ala Ala Phe Gly Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu
 1 5 10 15
 Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Arg Val Ile Arg
 20 25 30

<210> SEQ ID NO 90
 <211> LENGTH: 25
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 90
 Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly Ser Pro
 1 5 10 15
 His Tyr Ala Cys Pro Glu Val Ile Arg
 20 25

<210> SEQ ID NO 91
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 91


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Phe Leu Gln Thr Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile
1          5          10          15
Val Asn Gly Lys
          20
<210> SEQ ID NO 92
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 92
Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
1          5          10          15
Gln Gly Lys
<210> SEQ ID NO 93
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 93
Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly Ser Leu Ala Tyr
1          5          10          15
Ala Ala Pro Glu Leu Ile Gln Cys Lys
          20          25
<210> SEQ ID NO 94
<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: Schizosaccharomyces pombe
<400> SEQUENCE: 94
Met Ser Phe Leu Phe Asn Lys Arg Pro Lys Ser Thr Gln Asp Val Val
1          5          10          15
Arg Cys Leu Cys Asp Asn Leu Pro Lys Leu Glu Ile Asn Asn Asp Lys
          20          25          30
Lys Lys Ser Phe Glu Glu Val Ser Lys Cys Leu Gln Asn Leu Arg Val
          35          40          45
Ser Leu Cys Gly Thr Ala Glu Val Glu Pro Asp Ala Asp Leu Val Ser
          50          55          60
Asp Leu Ser Phe Gln Ile Tyr Gln Ser Asn Leu Pro Phe Leu Leu Val
          65          70          75          80
Arg Tyr Leu Pro Lys Leu Glu Phe Glu Ser Lys Lys Asp Thr Gly Leu
          85          90          95
Ile Phe Ser Ala Leu Leu Arg Arg His Val Ala Ser Arg Tyr Pro Thr
          100          105          110
Val Asp Tyr Met Leu Ala His Pro Gln Ile Phe Pro Val Leu Val Ser
          115          120          125
Tyr Tyr Arg Tyr Gln Glu Val Ala Phe Thr Ala Gly Ser Ile Leu Arg
          130          135          140
Glu Cys Ser Arg His Glu Ala Leu Asn Glu Val Leu Leu Asn Ser Arg
          145          150          155          160
Asp Phe Trp Thr Phe Phe Ser Leu Ile Gln Ala Ser Ser Phe Asp Met
          165          170          175
Ala Ser Asp Ala Phe Ser Thr Phe Lys Ser Ile Leu Leu Asn His Lys
          180          185          190
Ser Gln Val Ala Glu Phe Ile Ser Tyr His Phe Asp Glu Phe Phe Lys
          195          200          205
Gln Tyr Thr Val Leu Leu Lys Ser Glu Asn Tyr Val Thr Lys Arg Gln
          210          215          220
Ser Leu Lys Leu Leu Gly Glu Ile Leu Leu Asn Arg Ala Asn Arg Ser
          225          230          235          240
Val Met Thr Arg Tyr Ile Ser Ser Ala Glu Asn Leu Lys Leu Met Met

```

245
 Ile Leu Leu Arg Asp Lys Ser Lys Asn Ile Gln Phe Glu Ala Phe His
 260
 Val Phe Lys Leu Phe Val Ala Asn Pro Glu Lys Ser Glu Glu Val Ile
 275
 Glu Ile Leu Arg Arg Asn Lys Ser Lys Leu Ile Ser Tyr Leu Ser Ala
 290
 Phe His Thr Asp Arg Lys Asn Asp Glu Gln Phe Asn Asp Glu Arg Ala
 305
 Phe Val Ile Lys Gln Ile Glu Arg Leu
 325

<210> SEQ ID NO 95

<211> LENGTH: 399

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 95

Met Phe Lys Lys Tyr Lys Asn Gln Asp Leu Asp Met Ala Phe Trp Trp
 1
 Lys Lys Asn Pro Lys Thr Pro Ser Asp Tyr Ala Arg Leu Ile Ile Glu
 20
 Gln Leu Asn Lys Phe Ser Ser Pro Ser Leu Thr Gln Asp Asn Lys Arg
 35
 Lys Val Gln Glu Glu Cys Thr Lys Tyr Leu Ile Gly Thr Lys His Phe
 50
 Ile Val Gly Asp Thr Asp Pro His Pro Thr Pro Glu Ala Ile Asp Glu
 65
 Leu Tyr Thr Ala Met His Arg Ala Asp Val Phe Tyr Glu Leu Leu Leu
 85
 His Phe Val Asp Leu Glu Phe Glu Ala Arg Arg Glu Cys Met Leu Ile
 100
 Phe Ser Ile Cys Leu Gly Tyr Ser Lys Asp Asn Lys Phe Val Thr Val
 115
 Asp Tyr Leu Val Ser Gln Pro Lys Thr Ile Ser Leu Met Leu Arg Thr
 130
 Ala Glu Val Ala Leu Gln Lys Gly Cys Gln Asp Ile Phe Leu Thr
 145
 Val Gly Asn Met Ile Ile Glu Cys Ile Lys Tyr Glu Gln Leu Cys Arg
 165
 Ile Ile Leu Lys Asp Pro Gln Leu Trp Lys Phe Phe Glu Phe Ala Lys
 180
 Leu Gly Asn Phe Glu Ile Ser Thr Glu Ser Leu Gln Ile Leu Ser Ala
 195
 Ala Phe Thr Ala His Pro Lys Leu Val Ser Lys Glu Phe Phe Ser Asn
 210
 Glu Ile Asn Ile Ile Arg Phe Ile Lys Cys Ile Asn Lys Leu Met Ala
 225
 His Gly Ser Tyr Val Thr Lys Arg Gln Ser Thr Lys Leu Ala Ser
 245
 Leu Ile Val Ile Arg Ser Asn Asn Ala Leu Met Asn Ile Tyr Ile Asn
 260
 Ser Pro Glu Asn Leu Lys Leu Ile Met Thr Leu Met Thr Asp Lys Ser
 275
 Lys Asn Leu Gln Leu Glu Ala Phe Asn Val Phe Lys Val Met Val Ala
 290
 Asn Pro Arg Lys Ser Lys Pro Val Phe Asp Ile Leu Val Lys Asn Arg
 305
 Asp Lys Leu Leu Thr Tyr Phe Lys Thr Phe Gly Leu Asp Ser Gln Asp
 320

325 330 335
 Ser Thr Phe Leu Asp Glu Arg Glu Phe Ile Val Gln Glu Ile Asp Ser
 340 345 350
 Leu Pro Arg Ile Ile Ser Ser Thr Thr Glu Val Ser Asn Asn Asn Ala
 355 360 365
 Ser Ser Ser Asn Val Ala Ser Ile Thr Ser Pro Ser Ser Val Met Asn
 370 375 380
 Asn Gln Ser Ser Ile Leu Thr His Ser Thr Ser Pro Asp Ser Arg
 385 390 395

<210> SEQ ID NO 96

<211> LENGTH: 343

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 96

Met Arg Gly Leu Phe Lys Ser Lys Pro Arg Thr Pro Ala Asp Ile Val
 1 5 10 15
 Arg Gln Thr Arg Asp Leu Leu Leu Tyr Ala Asp Arg Ser Asn Ser Phe
 20 25 30
 Pro Asp Leu Arg Glu Ser Lys Arg Glu Lys Met Val Glu Leu Ser
 35 40 45
 Lys Ser Ile Arg Asp Leu Lys Leu Ile Leu Tyr Gly Asn Ser Glu Ala
 50 55 60
 Glu Pro Val Ala Glu Ala Cys Ala Gln Leu Thr Gln Glu Phe Phe Lys
 65 70 75 80
 Ala Asp Thr Leu Arg Arg Leu Leu Thr Ser Leu Pro Asn Leu Asn Leu
 85 90 95
 Glu Ala Arg Lys Asp Ala Thr Gln Val Val Ala Asn Leu Gln Arg Gln
 100 105 110
 Gln Val Asn Ser Arg Leu Ile Ala Ala Asp Tyr Leu Glu Ser Asn Ile
 115 120 125
 Asp Leu Met Asp Phe Leu Val Asp Gly Phe Glu Asn Thr Asp Met Ala
 130 135 140
 Leu His Tyr Gly Thr Met Phe Arg Glu Cys Ile Arg His Gln Ile Val
 145 150 155 160
 Ala Lys Tyr Val Leu Asp Ser Glu His Val Lys Lys Phe Phe Tyr Tyr
 165 170 175
 Ile Gln Leu Pro Asn Phe Asp Ile Ala Ala Asp Ala Ala Thr Phe
 180 185 190
 Lys Glu Leu Leu Thr Arg His Lys Ser Thr Val Ala Glu Phe Leu Ile
 195 200 205
 Lys Asn Glu Asp Trp Phe Phe Ala Asp Tyr Asn Ser Lys Leu Leu Glu
 210 215 220
 Ser Thr Asn Tyr Ile Thr Arg Arg Gln Ala Ile Lys Leu Leu Gly Asp
 225 230 235 240
 Ile Leu Leu Asp Arg Ser Asn Ser Ala Val Met Thr Lys Tyr Val Ser
 245 250 255
 Ser Met Asp Asn Leu Arg Ile Leu Met Asn Leu Leu Arg Glu Ser Ser
 260 265 270
 Lys Thr Ile Gln Ile Glu Ala Phe His Val Phe Lys Leu Phe Val Ala
 275 280 285
 Asn Gln Asn Lys Pro Ser Asp Ile Ala Asn Ile Leu Val Ala Asn Arg
 290 295 300
 Asn Lys Leu Leu Arg Leu Leu Ala Asp Ile Lys Pro Asp Lys Glu Asp
 305 310 315 320
 Glu Arg Phe Asp Ala Asp Lys Ala Gln Val Val Arg Glu Ile Ala Asn
 325 330 335
 Leu Lys Leu Arg Glu Leu Ala

340

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<210> SEQ ID NO 97
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: FLAG peptide
<400> SEQUENCE: 97
    Asp Tyr Lys Asp Asp Asp Asp Lys
    1                               5
<210> SEQ ID NO 98
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Bovine MBP fragment
<400> SEQUENCE: 98
    Gly His His Ala Ala Arg Thr Thr His Tyr Gly Ser Leu Pro Gln
    1                               5               10               15
<210> SEQ ID NO 99
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 99
    ggatccgccca ccatggagca gaagctgac tctgaagagg acttgccgtt cccgtttggg
    aagtttcaca aat
    60
    73
<210> SEQ ID NO 100
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 100
    ggatccttaa gcttcttgct gagctggtct cttc
    34
<210> SEQ ID NO 101
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 101
    caccggatcc gccaccatgg agcagaagct gatctctgaa gaggacttgc ctttgtttag
    taaatcacac aaaaatcc
    60
    78
<210> SEQ ID NO 102
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 102
    ggatcctcaa ggggccgttt tcttcaagtc tcgg
    34
<210> SEQ ID NO 103
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial

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<220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 103
 ggatccgcca ccatggacta caaggacgac gatgacaagt catttctgt aagtaaacca 60
 gagcgaatc 69
 <210> SEQ ID NO 104
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 104
 ggatcctcag aactcccaat cgtccacctc cagct 35
 <210> SEQ ID NO 105
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 105
 ggatccgcca ccatggacta caaggacgac gatgacaagt ctcttttggga ttgcttctgc 60
 acttcaag 68
 <210> SEQ ID NO 106
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 106
 ggatccctag aattcccagt atgagtcttt ttcac 36
 <210> SEQ ID NO 107
 <211> LENGTH: 66
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 107
 actagtgcca ccatggacta caaggacgac gatgacaaga agctcatcgg caagtacctg 60
 atgggg 66
 <210> SEQ ID NO 108
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer
 <400> SEQUENCE: 108
 actagttcag tctccaggt agggcactac agtcac 36
 <210> SEQ ID NO 109
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 109
 Cys Asp Pro Met Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu
 1 5 10
 <210> SEQ ID NO 110
 <211> LENGTH: 22
 <212> TYPE: PRT

<213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 110
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Arg Arg Arg
 20
 <210> SEQ ID NO 111
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Rattus rattus
 <400> SEQUENCE: 111
 Lys Phe Leu Arg Thr Ser Cys Gly Ser Pro Asn Tyr Ala
 1 5 10
 <210> SEQ ID NO 112
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 112
 actgcagccc tggagcccg gaagc 25
 <210> SEQ ID NO 113
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 113
 ctagttgagc ttgctgcaga tctccagcgc 30
 <210> SEQ ID NO 114
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 114
 actagtgcga ccatgtaccc atacgatgtg ccagattacg ccgaaggggc cgccgcgcct 60
 gtggcgggg 69
 <210> SEQ ID NO 115
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 115
 ctagttgagc ttgctgcaga tctccagcgc 30
 <210> SEQ ID NO 116
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 116
 actagtgcga ccatgtaccc atacgatgtg ccagattacg ccgagtcgct ggttttcgcg 60
 cggcgctcc 69
 <210> SEQ ID NO 117
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 117
 tcaggtgagc tttgagcaga ccctcagtgc ctg 33
 <210> SEQ ID NO 118
 <211> LENGTH: 55
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 118
 gcgtcgacta cccatcagat gtgccagatt acgcgctcat ggcggatggc ccgag 55

<210> SEQ ID NO 119
 <211> LENGTH: 55
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 119
 gcactagtta cccatacgat gtgccagatt acgccgtcat ggcggatggc ccgag 55

<210> SEQ ID NO 120
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 120
 gagcggcgcc taattcacca ggacataccc gttgtg 36

<210> SEQ ID NO 121
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 121
 gcggatccta cccatacgat gtgccagatt acgccgttat catgtcggag ttcagcgcg 60

<210> SEQ ID NO 122
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 122
 gagcggcgcc tcaactgcacc aggacaaacg tgcc 34

<210> SEQ ID NO 123
 <211> LENGTH: 75
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 123
 gcggatccta cccatacgat gtgccagatt acgccaaga ttatgatgaa cttctcaa 60
 attatgaatt acatg 75

<210> SEQ ID NO 124
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 124
 gtgcggcgcc ttataccttg cagctagata ggatgtcttc c 41

<210> SEQ ID NO 125
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 125
 ccacccccac ccacccccagc acgccaata tgtggggccc tatcgggtgg agaagacgct 60
 gggcaagg 69

<210> SEQ ID NO 126
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 126
 cgatgcagcc tctcgcggtc cctgaagcag c 31

<210> SEQ ID NO 127
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 127
 gctgtctcag ggaccgcgag aggtgtcatc g 31

<210> SEQ ID NO 128

<211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 128
 tcagggcaga ggggtcccgt tgggtggcc 28
 <210> SEQ ID NO 129
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 129
 ggtgggggct ctcccgccta ccacctcccc cacccccacc ccaaccacc ccagcacggc 60
 caatatg 67
 <210> SEQ ID NO 130
 <211> LENGTH: 76
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 130
 ggatcctacc catacgtatg gccagattac gcctcgtccg gggccaagga gggaggtggg 60
 ggctctcccg cctacc 76
 <210> SEQ ID NO 131
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 131
 gcggataccta cccatacgat gtgcc 25
 <210> SEQ ID NO 132
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 132
 ggatccgcca ccatgtaccc atacgatgtg ccagattacg ccacatcgac ggggaaggac 60
 ggcggcgcg 69
 <210> SEQ ID NO 133
 <211> LENGTH: 57
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 133
 gcggccgctc agaggctact ctctgtagctg gtggccacct tctggccctt aagccca 57
 <210> SEQ ID NO 134
 <211> LENGTH: 90
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 134
 ggagccgggc ccgcgggcgc cctgctgctt ccgcccggcg cggggtcccc agccgcccc 60
 gctgccgtgt ccctgcggc cggccagccg 90
 <210> SEQ ID NO 135
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 135
 tgaagaggtt actgaaacca aaatctgcta ttttgatatt c 41
 <210> SEQ ID NO 136
 <211> LENGTH: 87
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 136
 gattaccgcg cggcggcggc ggcgagcgga gctggcgggg ctgccggggc cgggactggg 60

ggagccgggc ccgcgggcgc cctgctg 87

<210> SEQ ID NO 137

<211> LENGTH: 55

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

gcggaacccta cccatacgat gtgccagatt acgcccgggc gccggcgccg agcgg 55

<210> SEQ ID NO 138

<211> LENGTH: 90

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

atagcagatt ttggtttcag taacctcttc actcctgggc agctgctgaa gacctgggtg 60

ggcagccctc cctatgctgc acctgaactc 90

<210> SEQ ID NO 139

<211> LENGTH: 34

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

ctgtggacat aaaaaatggg atgcggaact ttcc 34

<210> SEQ ID NO 140

<211> LENGTH: 34

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

ggaagtgtcc gcattccatt ttttatgtcc acag 34

<210> SEQ ID NO 141

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

gagcgccgc ttacacgctt gctgctcca tgc 33

<210> SEQ ID NO 142

<211> LENGTH: 54

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

gcgaattcta cccatacgat gtgccagatt acgcctcggc ccggacgccca ttgc 54

<210> SEQ ID NO 143

<211> LENGTH: 37

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

catcatactt ctgatttatt aaggcatcat ttatttc 37

<210> SEQ ID NO 144

<211> LENGTH: 37

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 144

gaaataaatg atgccttaat aaatcagaag tatgatg 37

<210> SEQ ID NO 145

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

gagtcgactt acagcttaag ctcatttget atttttgatg c 41

<210> SEQ ID NO 146

<211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 146
 gcggtacctta cccatacga gtgccagatt acgcctcggc cgggacgcca ttgc 54
 <210> SEQ ID NO 147
 <211> LENGTH: 43
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 147
 gagcgggcgc ttacagctta agctcatttg ctatttttga tgc 43
 <210> SEQ ID NO 148
 <211> LENGTH: 56
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 148
 gcgtcgacta cccatacga gtgccagatt acgccattcg gggccgcaac tcagcc 56
 <210> SEQ ID NO 149
 <211> LENGTH: 56
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 149
 gcactagtta cccatacga gtgccagatt acgccattcg gggccgcaac tcagcc 56
 <210> SEQ ID NO 150
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 150
 gagcgggcgc ttaaagcttc agctcgttgg ctatttttgg 39
 <210> SEQ ID NO 151
 <211> LENGTH: 73
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 151
 gcgccgcgag ccaccatgta cccatacga gtgccagatt acgcctccac taggacccca 60
 ttgccaacgg tga 73
 <210> SEQ ID NO 152
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 152
 gcgccgcgctt acagcttttag ctcatggca attttggaag c 41
 <210> SEQ ID NO 153
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 153
 agatctgcca ccatgtaccc atacgatgtg ccagattacg cctcttcgag gacggtgctg 60
 gccccggg 68
 <210> SEQ ID NO 154
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 154
 tgccctgaaa cagctccggg gcggc 25
 <210> SEQ ID NO 155
 <211> LENGTH: 25

<212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 155
 gggatcgaag ctggacacgt tctgc 25
 <210> SEQ ID NO 156
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 156
 gcggccgctc acactccagg ggaatcggag cagccgggg 39
 <210> SEQ ID NO 157
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Artificial AMPK kinase substrate
 <400> SEQUENCE: 157
 Ala Met Ala Arg Ala Ala Ser Ala Ala Ala Leu Ala Arg Arg Arg
 1 5 10 15
 <210> SEQ ID NO 158
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 158
 Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 159
 <211> LENGTH: 377
 <212> TYPE: PRT
 <213> ORGANISM: Caenorhabditis elegans
 <400> SEQUENCE: 159
 Met Pro Leu Leu Phe Gly Lys Ser His Lys Ser Pro Ala Asp Val Val
 1 5 10 15
 Lys Thr Leu Arg Glu Val Leu Thr Ile Leu Asp Lys Leu Pro Pro Pro
 20 25 30
 Lys Leu Asp Lys Asp Gly Asn Ile Gln Ser Asp Lys Lys Tyr Asp Lys
 35 40 45
 Ala Leu Asp Glu Val Ser Lys Asn Val Ala Met Ile Lys Ser Phe Ile
 50 55 60
 Tyr Gly Asn Asp Ser Ala Glu Pro Ser Ser Glu His Val Val Gln Val
 65 70 75 80
 Ala Gln Leu Ala Gln Glu Val Tyr Asn Ala Asn Ile Leu Pro Met Leu
 85 90 95
 Ile Lys Met Leu Pro Lys Phe Glu Phe Glu Cys Lys Lys Asp Val Gly
 100 105 110
 Gln Ile Phe Asn Asn Leu Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
 115 120 125
 Thr Val Glu Tyr Leu Gly Ala Arg Pro Glu Ile Leu Ile Gln Leu Val
 130 135 140
 Gln Gly Tyr Ser Val Pro Asp Ile Ala Leu Thr Cys Gly Leu Met Leu
 145 150 155 160
 Arg Glu Ser Ile Arg His Asp His Leu Ala Lys Ile Ile Leu Tyr Ser
 165 170 175
 Asp Val Phe Tyr Thr Phe Phe Leu Tyr Val Gln Ser Glu Val Phe Asp
 180 185 190

